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GenCore version 4.5
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OM protein - protein search, using sw model

Run on:

March 9, 2001, 16:43:01 ; Search time 26.57 Seconds
(without alignments)
178.884 Million cell updates/sec

Title: US-09-203-768a-2
Perfect score: 748
Sequence: 1 MKHLWFFLLVAAAPRWLSQ ARPHRYFDYWGQGTLWTVSS 139

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_36:*

1: /\$IDS1/geodata/geneseq/geneseqp/AA1980.DAT:*

2: /\$IDS1/geodata/geneseq/geneseqp/AA1981.DAT:*

3: /\$IDS1/geodata/geneseq/geneseqp/AA1982.DAT:*

4: /\$IDS1/geodata/geneseq/geneseqp/AA1983.DAT:*

5: /\$IDS1/geodata/geneseq/geneseqp/AA1984.DAT:*

6: /\$IDS1/geodata/geneseq/geneseqp/AA1985.DAT:*

7: /\$IDS1/geodata/geneseq/geneseqp/AA1986.DAT:*

8: /\$IDS1/geodata/geneseq/geneseqp/AA1987.DAT:*

9: /\$IDS1/geodata/geneseq/geneseqp/AA1988.DAT:*

10: /\$IDS1/geodata/geneseq/geneseqp/AA1989.DAT:*

11: /\$IDS1/geodata/geneseq/geneseqp/AA1990.DAT:*

12: /\$IDS1/geodata/geneseq/geneseqp/AA1991.DAT:*

13: /\$IDS1/geodata/geneseq/geneseqp/AA1992.DAT:*

14: /\$IDS1/geodata/geneseq/geneseqp/AA1993.DAT:*

15: /\$IDS1/geodata/geneseq/geneseqp/AA1994.DAT:*

16: /\$IDS1/geodata/geneseq/geneseqp/AA1995.DAT:*

17: /\$IDS1/geodata/geneseq/geneseqp/AA1996.DAT:*

18: /\$IDS1/geodata/geneseq/geneseqp/AA1997.DAT:*

19: /\$IDS1/geodata/geneseq/geneseqp/AA1998.DAT:*

20: /\$IDS1/geodata/geneseq/geneseqp/AA1999.DAT:*

21: /\$IDS1/geodata/geneseq/geneseqp/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT	1
ID	R66324
DT	03-AUG-1995 (first entry)
DE	Human immunoglobulin variable heavy chain #30.
KW	primer; PCR; amplify; human; immunoglobulin; variable; heavy chain; cosmids; placenta; vector; pJB1; E.coli; mammalian.
OS	Homo sapiens.
XX	
PN	W09426895-A.
XX	
PD	24-NOV-1994.
XX	
PR	10-MAY-1993; 93WO-JP00603.
XX	
(NISB) JAPAN TOBACCO INC.	
PA	
XX	
PI	Honjo T, Matsuda F;
XX	
DR	WPI; 1995-006791/01.
DR	N-PSDB; Q78972.
XX	
PT	DNA fragment comprising human immunoglobulin Vh genes - for the
PT	production of human immunoglobulin in mammalian hosts
XX	
PS	Claim 41; Page 74-75; 130pp; Japanese.
XX	

1	622	83.2	115	16	R66324	Human immunoglobul	Primateised anti-hu
2	588	78.6	139	21	Y82628	Human PTTRP monocl	Macaque primatized
3	580	77.5	139	21	Y64676	Human 5' EST relat	Human immune syste
4	575.5	76.9	472	17	R93165	Anti-rhesus D rec	Human immunoglobul
5	566	75.7	244	20	Y21883	Amino acid sequenc	Monoclonal antibod
6	560.5	74.9	136	18	W24536	Immunglobulin rB6	Human immunoglobul
7	558.5	74.7	123	17	W03757	Anti-rhesus D mono	Anti-CD4 cynomolg
8	558.5	74.7	142	14	R41285	F105 rearranged va	Monkey anti-CD4 he
9	552	73.8	128	12	R12269	Anti-human RHD FOM	Amino acid sequenc
10	550	73.5	116	14	R42689	Vh 71-4. Homo sap	Anti-CD4 VH peptid
11	550	73.5	116	16	R66346	Human immunoglobul	Human gamma-4' peptid
12	543	72.6	141	21	Y56728	Amino acid sequenc	Human gamma-4' heavy

protein sequences (R66295-51) are novel human immunoglobulin heavy chain sequences encoded by novel isolated genes. The genes (Q78939-79002) were isolated and cloned from a series of cDNA constructs: Y202; Y103; Y21; Y6; Y24; 3-31; M84; M118 and M311, by PCR amplification using primers Q78917-38. The genes are subdivided into 5 families of Vh genes. The fragments cover a region of 800 kb. The DNA fragments were isolated from high molecular weight DNA from human placenta. The DNA was partially digested with TaqI restriction enzyme. The fragments were separated by gel electrophoresis and 35-45 kb fractions were collected. The fragments were ligated with ClaI-digested cosmid vector pJBB1. The ligation products were then subcloned by colony hybridisation. The Vh genes and the DNA fragments encoding them are useful in producing human immunoglobulin in mammalian hosts.

SQ Sequence 116 AA;

Query Match 83.2%; Score 622; DB 16; Length 116;
Best Local Similarity 100.0%; Pred. No. 8.5e-45; Mismatches 0; Indels 0; Gaps 0;
Matches 116; Conservative 0; MisMatches 0;

QY 1 MKHLWFLLLVAAPRVLSQLQVQLOQNGAGLKKPSETLSLTCAVVGGFSSYYWSNIRQPP 60
Db 1 mkhlfllvaaaptwvlsqyq1qwgaglkpksetlsitcavvqggsfyywswirqpp 60

QY 61 GKGWLWIGEINHSGSTNYNPSLKSRTVISTDSKQFSKLSSVTAADTAWYYCAREIA 116
Db 61 gkglewigiyysgstsxynpksksrtvistdskqfsklssvtaadtwyycasavy 116

RESULT 2

Y82628
ID Y82628 standard; Protein; 139 AA.

AC XX
XX Y82628;
XX DT 02-AUG-2000 (first entry)
DE Human PTHrP monoclonal antibody clone 4B4-6-21 protein SEQ ID NO:40.
XX KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
KW hypercalcemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
KW sepsis; systemic inflammatory response syndrome; SIRS;
KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
OS Homo sapiens.

KEY Location/Qualifiers

FH Misc-difference 77
FT /note= "possibly Tyr"
XX JP2000080100-A.
XX PD 21-MAR-2000.
XX PP 12-OCT-1998; 98JP-0304793.
XX PR 17-JUN-1998; 98JP-0188196.
XX PR 26-JUN-1998; 98JP-0196729.
XX PA (NISB) JAPAN TOBACCO INC.
DR N-PSDB; A13938.

XX A human monoclonal antibody to parathyroid hormone related protein. -

PT useful for treating hypercalcemia, rheumatoid arthritis, cancer of bone
PT including metastasis, and pain

XX Claim 32; Page 75; 88pp; Japanese.

protein sequences (R66295-51) are novel human immunoglobulin heavy chain sequences encoded by novel isolated genes. The genes (Q78939-79002) were isolated and cloned from a series of cDNA constructs: Y202; Y103; Y21; Y6; Y24; 3-31; M84; M118 and M311, by PCR amplification using primers Q78917-38. The genes are subdivided into 5 families of Vh genes. The fragments cover a region of 800 kb. The DNA fragments were isolated from high molecular weight DNA from human placenta. The DNA was partially digested with TaqI restriction enzyme. The fragments were separated by gel electrophoresis and 35-45 kb fractions were collected. The fragments were ligated with ClaI-digested cosmid vector pJBB1. The ligation products were then subcloned by colony hybridisation. The Vh genes and the DNA fragments encoding them are useful in producing human immunoglobulin in mammalian hosts.

SQ Sequence 116 AA;

Query Match 83.2%; Score 622; DB 16; Length 116;
Best Local Similarity 100.0%; Pred. No. 8.5e-45; Mismatches 0; Indels 0; Gaps 0;
Matches 116; Conservative 0; MisMatches 0;

QY 1 MKHLWFLLLVAAPRVLSQLQVQLOQNGAGLKKPSETLSLTCAVVGGFSSYYWSNIRQPP 60
Db 1 mkhlfllvaaaptwvlsqyq1qwgaglkpksetlsitcavvqggsfyywswirqpp 60

QY 61 GKGWLWIGEINHSGSTNYNPSLKSRTVISTDSKQFSKLSSVTAADTAWYYCAREIA 120
Db 61 gkglewigiyysgstsxynpksksrtvistdskqfsklssvtaadtwyycasavy 120

QY 121 RPHRYEDYWGQCTLVSS 139
Db 121 yyygldvwqggttvlvss 139

RESULT 3

Y64676
ID Y64676 standard; Protein; 139 AA.

AC XX
XX Y64676;
XX DT 01-FEB-2000 (first entry)
DE Human 5' EST related polypeptide SEQ ID NO:837.

XX KW Human; 5' EST; expressed sequence tag; secreted protein; diagnosis;
KW gene therapy; chromosome mapping; upstream regulatory sequence;
KW forensic; location; development; protein synthesis; stability;
KW regulation; identification; regulation; identification.
XX OS Homo sapiens.
XX PN W0953051-A2.
XX PD 21-OCT-1999.
XX PP 09-APR-1999; 99WO-1B00712.
XX PR 09-APR-1998; 98US-0057719.
XX PR 28-APR-1998; 98US-0069047.
XX PA (GEST) GENSET.
XX Dumas Milne Edwards J, Ducleart A, Giordano J;
XX DR WPI; 2000-038446/03.
DR N-PSDB; 242290.

XX Novel secreted protein 5' expressed sequence tag sequences used in
PT diagnostic, forensic, gene therapy, and chromosome mapping procedures

XX Claim 3; Page 605-606; 83pp; English.
PS XX 242265 to 243075 represent novel 5' expressed sequence tag (EST)

The present invention describes a human monoclonal antibody to parathyroid hormone related protein (PTHrP). The monoclonal antibody or its fragments, following the stimulation of PTHrP has the following properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits the release of calcium from bone; or (c) inhibits elevation of blood calcium concentration. The monoclonal antibody can be used in the treatment of hypercalcemia, rheumatoid arthritis, cancer of bone including metastasis, pain, fracture, cachexia, diseases of teeth, periodontal diseases and gingiva, sepsis, systemic inflammatory response syndrome (SIRS), and hypophosphataemia. It has antiarthritic, cytostatic and antiinflammatory activities. The present sequence represents a human PTHrP monoclonal antibody clone protein sequence from the present invention.

SQ Sequence 139 AA;

Query Match 78.6%; Score 588; DB 21; Length 139;
Best Local Similarity 82.0%; Pred. No. 6.5e-42; Mismatches 5; Indels 0; Gaps 0;
Matches 114; Conservative 20; MisMatches 20;

QY 1 MKHLWFLLLVAAPRVLSQLQVQLOQNGAGLKKPSETLSLTCAVVGGFSSYYWSNIRQPP 60
Db 1 mkhlfllvaaaptwvlsqyq1qwgaglkpksetlsitcavvqggsfyywswirqpp 60

QY 61 GKGWLWIGEINHSGSTNYNPSLKSRTVISTDSKQFSKLSSVTAADTAWYYCAREIA 120
Db 61 gkglewigiyysgstsxynpksksrtvistdskqfsklssvtaadtwyycasavy 120

QY 121 RPHRYEDYWGQCTLVSS 139
Db 121 yyygldvwqggttvlvss 139

RESULT 4

Y64676
ID Y64676 standard; Protein; 139 AA.

AC XX
XX Y64676;
XX DT 01-FEB-2000 (first entry)
DE Human 5' EST related polypeptide SEQ ID NO:837.

XX KW Human; 5' EST; expressed sequence tag; secreted protein; diagnosis;
KW gene therapy; chromosome mapping; upstream regulatory sequence;
KW forensic; location; development; protein synthesis; stability;
KW regulation; identification; regulation; identification.
XX OS Homo sapiens.
XX PN W0953051-A2.
XX PD 21-OCT-1999.
XX PP 09-APR-1999; 99WO-1B00712.
XX PR 09-APR-1998; 98US-0057719.
XX PR 28-APR-1998; 98US-0069047.
XX PA (GEST) GENSET.
XX Dumas Milne Edwards J, Ducleart A, Giordano J;
XX DR WPI; 2000-038446/03.
DR N-PSDB; 242290.

XX Novel secreted protein 5' expressed sequence tag sequences used in
PT diagnostic, forensic, gene therapy, and chromosome mapping procedures

XX Claim 3; Page 605-606; 83pp; English.
PS XX 242265 to 243075 represent novel 5' expressed sequence tag (EST)

XX
PR 03-DEC-1997; 97US-0067428.
XX
PA (BOEFL) BOHRINGER MANNHEIM CORP.
XX
PT Mahoney W, Sawyer JR, Winter GP;
XX
DR WPI; 1999-432068/37.
XX
N-PSDB; X86940.

XX
PT New anti-complex antibody useful for diagnosing prostate cancer
XX
PS Claim 28; Page 25-27; 42pp; English.
XX
CC The invention relates to an antibody that binds a complex between
CC prostate-specific antigen (PSA) and anti-chymotrypsin (ACT) and has an
CC affinity for the complex which is at least 10 fold higher than the
CC affinity for either PSA or ACT alone. The antibody is used in diagnostic
CC assays to detect PSA-ACT in serum samples from patients. The levels of
CC PSA-ACT complex increase in patients suffering from prostate cancer
CC compared to the levels in patients with benign or no growths in the
CC prostate. Therefore detection of PSA in complex with ACT is useful for
CC the early detection of prostate tumours, by distinguishing between benign
CC and malignant conditions of the prostate as well as for the management of
CC patients with prostate cancer, such as the disclosure of metastasis and
CC the monitoring of the PSA levels after treatment. The antibodies may
CC also be used in immunotherapy, affinity chromatography and isolation or
CC purification of PSA-ACT. Unlike prior art antibodies which bind to
CC PSA-ACT complexes but may also bind PSA or ACT alone, the present
CC antibody is specific for PSA-ACT alone. Diagnostic assays using the
CC antibodies are more accurate in diagnosing prostate cancer as they only
CC detect the intact complex of PSA-ACT. Sequences Y1880-884 represent
CC specific examples of antibodies directed against PSA-ACT. The present
CC sequence represents the amino acid sequenced of antibody B108.
XX
Sequence 244 AA;

Query Match 75.7%; Score 566; DB 20; Length 244;
Best Local Similarity 89.3%; Pred. No. 7.6e-40; Mismatches 109; Conservative 5; Indels 4; Gaps 1; Matches 109;

Qy 18 LSOVQDQWAGLPLPSETSLTCAVYGGGRGSGWYWSWIRQPPGKLEWGEINNSGSTN 77
Db 1 mklhwflilveaprwlsvqlqesggpkvlpksetlsitctvsgsdissyywswirqpp 60

Qy 78 YNPSIKSRVVISDPSKQSLKLSSVTAADTAVVYCAREIARHRYFWGQCLTVY 137
Db 61 ynpisksrvtsvdsknqfsklssvtaadtavyycareerg 120

Qy 138 SS 139
Db 117 ss 118

RESULT 6
W24536 ID W24536 standard; Protein: 136 AA.
XX
AC W24536;
XX
DT 09-OCT-1997 (first entry)
XX
DE Immunoglobulin heavy chain variable region.
XX
KW Immunoglobulin; variable region; heavy chain; thyrotropin receptor;
KW thyroid stimulating activity; light chain; Basedow's disease; antibody;
KW peripheral blood lymphocyte.
XX
OS Homo sapiens.
XX
FH Key Peptide
XX
FT Location/Qualifiers 1.19

FT Protein /note= "signal peptide" 20.136
XX
FT Protein 20.136
XX
PN JP09140386-A.
XX
PD 03-JUN-1997.
XX
PF 22-NOV-1995; 95JP-0328235.
XX
PR 22-NOV-1995; 95JP-0328235.
XX
PA (EIKE) EIKEN KAGAKU KK.
XX
DR WPI; 1997-344899/32.
XX
N-PSDB; T79919.

XX
PT Antibody containing immunoglobulin heavy chain mutation - with
PT thyroid function stimulating activity
XX
PS Claim 31; Page 14-15; 18pp; Japanese.

Query Match 74.9%; Score 560.5; DB 18; Length 136;
Best Local Similarity 81.6%; Pred. No. 1.2e-39; Mismatches 111; Conservative 4; Indels 3; Gaps 2; Matches 111;

Qy 1 MKHLWFLLVVAAPRVLWSQVQLOQWAGLPLPSETSLTCAVYGGSGFSSYYWSWIRQPP 60
Db 1 mklhwflilveaprwlsvqlqesggpkvlpksetlsitctvsgsdissyywswirqpp 60

Qy 61 GKGLEMIGEHHSGSYNNSILKSRTVTSKNOFSKLSSVVAADTAVVYCAREI- 118
Db 61 gkglewigiybhsyngstnssilksrvtsvdsknqfsklssvtaadtavyycareerg 120

Qy 119 AARPHRY-FDWGQGT 133
Db 121 91rdfaygmawqggt 136

RESULT 7
W03757 ID W03757 standard; Protein: 123 AA.
XX
AC W03757;
XX
DT 29-OCT-1996 (first entry)
XX
DE Anti-rhesus D monoclonal antibody D7C2 heavy chain V region.
XX
KW Human monoclonal antibody; immunoglobulin isotype IgM; agglutination;
KW rhesus positive; rhesus negative; haemolysis; heavy chain;
KW variable region; insect host cell; baculovirus; recombinant production.
XX
OS Homo sapiens.
XX
FT Key Location/Qualifiers
FT Region 29..35
FT /label= CDR1
FT /note= "complementarity determining region"
FT Region 50..65
FT /label= CDR2

FT	Key	Location/Qualifiers
FT	Region	31..35 /label= CDR1
FT	Region	50..65 /label= CDR2
FT	Region	98..117 /label= CDR3
PN	W09107492-A.	
XX	30-MAY-1991.	
XX	30-MAY-1991.	
PF	WPI: 1991-178104/24.	
XX	13-NOV-1989; 89GBB-0025590.	
XX	(BLCO-) CENT BLOOD LAB AUTH.	
PA	Hughes - Jones N;	
XX	WPI: 1991-178104/24.	
DR	N-PSDB; Q11951.	
XX	PT DNA encoding complementary determining regions - of human anti-rhesus D antibodies, useful in prodn. of monoclonal antibodies and for passive immunisation	
PS	PT Disclosure; Fig 8; 32pp; English.	
XX	CC The DNA sequence of eleven monoclonal antibodies are represented in Q19145-57. Synthetic genes, for both heavy and light chains may be created by combining selected CDR 1, 2, and 3 regions, which may be selected from different antibody mols, having varied binding specificity. The chimaeric anti-RhD antibodies can be used for diagnosis and therapy, and are capable of providing blood-typing reagents of high specificity and reliability. They can also be used in passive immunisation to prevent haemolytic disease of the newborn.	
CC	CC Sequence 128 AA;	
SQ	Query Match 73.8%; Score 552; DB 12; Length 128; Best Local Similarity 83.7%; Pred. No. 5.7e-39; Matches 108; Conservative 4; Mismatches 7; Indels 10; Gaps 2;	
QY	20 QYOLQONGAGLKLKPSETSLTCAVYGGSSGYWWSIROPKGKLEWEIGEINHSGSTNRY 79	
Db	1 qyqkqpgaglkpsetsltcavyggssgywwsiropkgklewieginstnry 60	
QY	80 PSLKSRVITSVTSKNOFLKLSSVTAADTAVVYCARPHR-----YFDYNG 130	
Db	61 pslksvrtmsvtskqfskllssvtaadtvavycargl-erpirnqlrlgymdwg 119	
QY	131 QGTLVTVSS 139	
Db	120 kgtttvvtvss 128	
RESULT	10	
R42689	R42689 standard; Protein; 116 AA.	
XX		
AC	R42689;	
XX		
DT	01-NOV-1993 (first entry)	
DE	Vh 71-4.	
RESULT	11	
R66346	R66346 standard; Protein; 116 AA.	
ID		
XX		
AC	R66346;	
XX		
DT	04-AUG-1995 (first entry)	
XX		
DE	Human immunoglobulin variable heavy chain #52.	
XX		
KW	Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain; cosmid; placenta; vector; pJBB1; E.coli; mammalian.	
KW		
OS	Homo sapiens.	
FT	Key	Location/Qualifiers
FT	Peptide	1..19
FT	Protein	/label= sig-peptide
FT	Region	20..116
FT	Region	49..54
FT	Region	69..84
FT	Region	/label= mat_protein
FT	Region	/label= CDR1
FT	Region	/label= CDR2
PN	W09312232-A.	
XX	24-JUN-1993.	
XX	10-DEC-1992; 92WO-US10928.	
XX	10-DEC-1991; 91US-0804652.	
XX	PA (DAND) DANA FARBER CANCER INST INC.	
XX	PA (NEWE) NEW ENGLAND DEACONNESS HOSPITAL CORP.	
PT	Haseltine WA, Marasco WA, Posner MR, Sodroski JG;	
XX	DR WPI: 1993-214174/26.	
XX	DR N-PSDB; Q42697.	
XX	PT DNA segments encoding monoclonal antibody - which binds to gp120 and neutralises HIV, for treating AIDS, and for diagnosing and monitoring HIV infection	
PS	PT Disclosure; Page 64; 109pp; English.	
XX	CC The nucleotide sequence of rearranged F105 Vh (Q42698) was compared to two monoclonal antibodies (Ab26 - 042702) and 268-D - 042703, which by nucleotide sequence analysis, appear to use a rearranged Vh 71-4 gene (Q42697).	
CC	CC Ab26 (042702) was derived from CD5+ B cells of a healthy donor and represents a naturally occurring polyreactive antibody which binds to many antigens. Ab26 shares greatest sequence similarity with germline Vh 71-4.	
CC	CC Sequence 116 AA;	
SQ	Query Match 73.5%; Score 550; DB 14; Length 116; Best Local Similarity 90.5%; Pred. No. 7.5e-39; Matches 105; Conservative 3; Mismatches 8; Indels 0; Gaps 0; Gaps 0;	
QY	1 MKHLWFLFLVAPRWLQVQVQWAGLKLKPSETSLTCAVYGGSSGYWWSIROP 60	
Db	1 mkhlfwfllyvaprwlvsqvqlqespglpvlpstisltctvsgsryyywswirqpp 60	
QY	61 GKGLEWIGEINHSGSTNYPNSLKSRTVLSVDTSKNOFLKLSSVTAADTAVVYCAR 116	
Db	61 gkglewigiyysgnsynpslksrtvlsvdtksnqfskllssvtaadtvavycar 116	

XX
PN WO9426895-A.
XX
PD 24-NOV-1994.
XX
PF 10-MAY-1993; 93WO-JP00603.
PR 10-MAY-1993; 93WO-JP00603.
XX
PA (NISB) JAPAN TOBACCO INC.
XX
PI Honjo T, Matsuda F;
XX
DR WPI: 1995-006791/01.
DR N-PSDB; Q78997.
XX
PT DNA fragment comprising human immunoglobulin VH genes - for the
PT production of human immunoglobulin in mammalian hosts
XX
PS Disclosure; Page 107-108; 130pp; Japanese.
XX
CC Protein sequences (R66295-51) are novel human immunoglobulin heavy chain
CC sequences encoded by novel isolated genes. The genes (Q78939-79002) were
CC isolated and cloned from a series of cosmid constructs: Y202; Y103; Y21;
CC Y6; Y24; 3-31; M84; M118 and M131, by PCR amplification using primers
CC Q78917-38. The genes are subdivided into 5 families of VH genes. The
CC fragments cover a region of 800 kb. The DNA fragments were isolated from
CC high molecular weight DNA from human placenta. The DNA was partially
CC digested with TagI restriction enzyme. The fragments were separated by
CC gel electrophoresis and 35-45 kb fractions were collected. The fragments
CC were ligated with ClaI-digested cosmid vector pNB81. The ligation
CC products were in vitro packed and infected into E. coli 490A. The
CC fragments were then subcloned by colony hybridisation. The VH genes and
CC the DNA fragments encoding them are useful in producing human
XX
SQ Sequence 116 AA:

Query Match 73.5%; Score 550; DB 16; Length 116;
Best Local Similarity 90.5%; Pred. No. 7.5e-39; Indels 0; Gaps 0;
Matches 105; Conservative 3; Mismatches 8;

Qy 1 MKHLWFLLVAAPRWLSQLVQLOQWAGAGLKPSETLSLTCAVVGGFSFCYWSMIRQPP 60
Db 1 mkhlfllflvllaaprwlvqlsqvqpgspqjlpksetlsitctvsgsfsyywswirqpp 60

Qy 61 GKGLEWIGEINHSGSN-TRYNPSLKSRTVSDTSKQFSKLLSSVTAADTAVYCCAR 116
Db 61 gkglewigiyiyysstnypsklsrvtsvdatkskqfsklssvtaadtvyyccar 116

RESULT 12
ID Y56728 standard; protein; 141 AA.
XX
AC Y56728;
XX
DT 15-FEB-2000 (first entry)
XX
DE Amino acid sequence of Cynomologous VH cDNA clone 2-5.
XX
KW Complementarity determining region; antibody; primate; immunogenicity;
KW Old World ape; Old World monkey; antigen-binding affinity.
XX
OS Macaca cynomologus.
XX
PN WO955369-A1.
XX
PD 04-NOV-1999.
XX
PF 28-APR-1999; 99WO-US09131.
XX

Query Match 73.5%; Score 550; DB 16; Length 116;
Best Local Similarity 90.5%; Pred. No. 7.5e-39; Indels 0; Gaps 0;
Matches 105; Conservative 3; Mismatches 8;

Qy 1 MKHLWFLLVAAPRWLSQLVQLOQWAGAGLKPSETLSLTCAVVGGFSFCYWSMIRQPP 60
Db 1 mkhlfllflvllaaprwlvqlsqvqpgspqjlpksetlsitctvsgsfsyywswirqpp 60

Qy 61 GKGLEWIGEINHSGSN-TRYNPSLKSRTVSDTSKQFSKLLSSVTAADTAVYCCAREIA 119
Db 61 gkglewigiyiyysstnypsklsrvtsvdatkskqfsklssvtaadtvyyccardg 120

RESULT 13
ID W01822
ID W01822 standard; Protein; 476 AA.
XX
AC W01822;
XX
DT 25-MAY-1997 (first entry)
XX
DE Primate anti-human B7.1 antigen antibody 16C10 heavy chain.
XX
KW Monoclonal antibody; cynomolgus monkey; macaque; 16C10;
KW primatised antibody; B7 antigen; CD28; immunosuppressive;
KW autoimmune disease; idiopathic thrombocytopenia purpura;
KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW type 1 diabetes mellitus; graft versus host disease;
KW hetero-hybridoma; transfectoma.
XX
OS Chimeric Macaca cynomolgus;
OS Chimeric Homo sapiens.
DN WO9600878-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US10053.
XX
FR 07-JUN-1995; 95US-0487550.
XX

PR 28-APR-1998; 98US-0083367.
XX
(SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Taylor AH;
PR
DR WPI: 2000-023265/02.
N-PSDB; Z39331.
XX
PT Antibodies containing donor complementarity determining regions and
PT non-human primate acceptor frameworks, having reduced immunogenicity in
humans -
PR
DR
PS Example 3; Page 79; 123pp; English.
XX
CC The invention provides an antibody (Ab) comprising donor CDRs
CC (complementarity determining regions) derived from a non-human antigen-
CC specific donor antibody, and an acceptor framework from a non-human
CC primate. The Abs are prepared by grafting CDRs from a non-human antigen-
CC specific donor antibody onto homologous Old World ape or monkey acceptor
CC frameworks. The Abs have reduced immunogenicity and are better tolerated
CC in humans (because of the close similarity between the human and primate
CC proteins), but retain the full antigen-binding affinity of the donor
CC antibody.
XX
SQ Sequence 141 AA;

Query Match 72.6%; Score 543; DB 21; Length 141;
Best Local Similarity 75.2%; Pred. No. 3.5e-38; Indels 2; Gaps 2;
Matches 106; Conservative 10; Mismatches 23; Indels 2; Gaps 2;

Qy 1 MKHLWFLLVAAPRWLSQLVQLOQWAGAGLKPSETLSLTCAVVGGFSFCYWSMIRQPP 60
Db 1 mkhlfllflvllaaprwlvqlsqvqpgspqjlpksetlsitctvsgsfsyywswirqpp 60

Qy 61 GKGLEWIGEINHSGSN-TRYNPSLKSRTVSDTSKQFSKLLSSVTAADTAVYCCAREIA 119
Db 61 gkglewigiyiyysstnypsklsrvtsvdatkskqfsklssvtaadtvyyccardg 120

RESULT 14
ID W01822
ID W01822 standard; Protein; 476 AA.
XX
AC W01822;
XX
DT 25-MAY-1997 (first entry)
XX
DE Primate anti-human B7.1 antigen antibody 16C10 heavy chain.
XX
KW Monoclonal antibody; cynomolgus monkey; macaque; 16C10;
KW primatised antibody; B7 antigen; CD28; immunosuppressive;
KW autoimmune disease; idiopathic thrombocytopenia purpura;
KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW type 1 diabetes mellitus; graft versus host disease;
KW hetero-hybridoma; transfectoma.
XX
OS Chimeric Macaca cynomolgus;
OS Chimeric Homo sapiens.
DN WO9600878-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US10053.
XX
FR 07-JUN-1995; 95US-0487550.
XX

Int. Immunol. 3, 865-875, 1991
 A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and high-affinity immunoglobulin E receptors
 A;Reference number: S23716; MUID:92031262
 A;Accession: S23717
 A;Molecule type: mRNA
 A;Residues: 151-111 <HAW>
 A;Cross-references: EMBL:X5441
 C;Superfamily: immunoglobulin
 C;Keywords: immunoglobulin
 F;1-14/Domain: signal sequence (fragment) #status predicted <SIG>
 F;1-14/Domain: Ig heavy chain (fragment) #status predicted <SIG>
 F;29-111/Domain: immunoglobulin homology <IMM>

Query Match 85.7%; Score 641; DB 2; Length 140;
 Best Local Similarity 88.7%; Pred. No. 1.1e-50; Matches 126; Conservative 1; Mismatches 5; Indels 10; Gaps 2;
 Matches 126; Conservative 1; Mismatches 5; Indels 10; Gaps 2;
 QY 6 FFLILIVAAPRNLVLSQVOLQOWGAGLILKPSETLSLTCAVVGGSGFSGYYWMSWIROPGKGLIE 65
 Db 1 FFLILIVAAPRNLVLSQVOLQOWGAGLILKPSETLSLTCAVVGGSGFSGYYWMSWIROPGKGLIE 60
 QY 66 WIGENHNSCTNYNSLSKSRVTISDTSKQFSKLSSVTAADTAVYCAR-----E 117
 Db 61 WIGENHNSCTNYNSLSKSRVTISDTSKQFSKLSSVTAADTAVYCAR-----E 120
 QY 118 IAARRHRYDYWGQGTLVWSS 139
 Db 121 WLYLPF-AFDYWGGQGTLVWSS 140

RESULT 3
 I37782
 Ig variable region (VDJ) (clone T23-9) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
 C;Accession: I37782; S25476
 R;Demaillet, C.; Chastagner, P.; These, J.; Zouali, M.
 Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
 A;Title: Somatic diversification in the heavy chain variable region genes expressed by B cells
 A;Reference number: A36816; MUID:94119917
 A;Accession: I37782
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-140 <RES>
 A;Cross-references: EMBL:X67906; PIDN:CAA48104.1; PID:933583
 C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
 F;46-128/Domain: immunoglobulin homology <IMM>

Query Match 83.6%; Score 625.5; DB 2; Length 140;
 Best Local Similarity 86.4%; Pred. No. 2.6e-49; Matches 121; Conservative 6; Mismatches 12; Indels 1; Gaps 1;
 Matches 121; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

QY 1 MKHLMFFLLVAAPRNLVLSQVOLQOWGAGLILKPSETLSLTCAVVGGSGFSGYYWMSWIROPP 60
 Db 1 MKHLMFFLLVAAPRNLVLSQVOLQOWGAGLILKPSETLSLTCAVVGGSGFSGYYWMSWIROPP 60
 QY 61 GKGLEWIGEINHNSCTNYNSLSKSRVTISDTSKQFSKLSSVTAADTAVYCARERA 120
 Db 61 GKGLEWIGEINHNSCTNYNSLSKSRVTISDTSKQFSKLSSVTAADTAVYCARERA 120
 QY 121 RPHRY-FDYWGQGTLVWSS 139
 Db 121 SWGRRYFDWQGQGTLVWSS 140

RESULT 4
 S31586
 Ig heavy chain V region - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

Query Match 78.7%; Score 589; DB 2; Length 139;
 Best Local Similarity 82.7%; Pred. No. 4.9e-46; Matches 115; Conservative 4; Mismatches 20; Indels 0; Gaps 0;
 Matches 115; Conservative 4; Mismatches 20; Indels 0; Gaps 0;
 QY 1 MKHLMFFLLVAAPRNLVLSQVOLQOWGAGLILKPSETLSLTCAVVGGSGFSGYYWMSWIROPP 60
 Db 1 MKHLMFFLLVAAPRNLVLSQVOLQOWGAGLILKPSETLSLTCAVVGGSGFSGYYWMSWIROPP 60
 QY 61 GKGLEWIGEINHNSCTNYNSLSKSRVTISDTSKQFSKLSSVTAADTAVYCARERA 120
 Db 61 GKGLEWIGEINHNSCTNYNSLSKSRVTISDTSKQFSKLSSVTAADTAVYCARERA 120
 QY 121 RPHRY-FDYWGQGTLVWSS 139
 Db 121 IRRAEADINQGQTLVWSS 139

RESULT 5
 S31676
 Ig heavy chain V region - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C;Accession: S31676
 R;Cuisinier, A.M.; Gauthier, L.; Boubil, L.; Fougerousse, M.; Tonnelle, C.
 submitted to the EMBL Data Library, June 1992
 A;Description: Mechanisms that generate human immunoglobulin diversity operate from t
 A;Reference number: S31585
 A;Accession: S31676
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-137 <RES>
 A;Cross-references: EMBL:Z14182; PIDN:CAA78551.1; PID:931032
 C;Superfamily: heterotetrramer; immunoglobulin V region; immunoglobulin homology <IMM>
 C;Keywords: heterotetrramer; immunoglobulin V region; immunoglobulin homology <IMM>
 F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 78.2%; Score 585; DB 2; Length 137;
 Best Local Similarity 82.9%; Pred. No. 1.1e-45; Matches 116; Conservative 4; Mismatches 16; Indels 4; Gaps 2;
 Matches 116; Conservative 4; Mismatches 16; Indels 4; Gaps 2;

QY 1 MKHLMFFLLVAAPRNLVLSQVOLQOWGAGLILKPSETLSLTCAVVGGSGFSGYYWMSWIROPP 60
 Db 1 MKHLMFFLLVAAPRNLVLSQVOLQOWGAGLILKPSETLSLTCAVVGGSGFSGYYWMSWIROPP 60
 QY 61 GKGLEWIGEINHNSCTNYNSLSKSRVTISDTSKQFSKLSSVTAADTAVYCARERA 120
 Db 61 GKGLEWIGEINHNSCTNYNSLSKSRVTISDTSKQFSKLSSVTAADTAVYCARERA 120
 QY 121 RPHRY-FDYWGQGTLVWSS 139
 Db 121 SWGRRYFDWQGQGTLVWSS 139

RESULT 6
 S13519
 Ig heavy chain V region precursor - human
 C;Species: Homo sapiens (man)

F;47-129/Domain: immunoglobulin homology <IMM>

Query Match 76.3%; Score 571; DB 2; Length 126;
 Best Local Similarity 87.3%; Pred. No. 1. 8e-44;
 Matches 110; Conservative 3; Mismatches 7; Indels 6; Gaps 1;

Y	20	QVOLQWGAGLKPSETSLTCATVGGSGFSGYWMWRQPPSKGLEINIGEINHGSTNYN	79
b	1	OVOLOQWGSAGLKPSETSLTCATVGGSGFSGYWMWRQPPSKGLEINIGEINHGSTNYN	60
b	80	PSLKSRTVTSVDTISKQNLKLSVTAAATDVVYCAR-----EAAPRPHRFYDWMQGQT	133
b	61	1 1 1 1 1 1 1 1 1 1 1	120
b	134	PSLKSRTVTSVDTISKQNLKLSVTAAATDVVYCARGGQCPKKASCYTKNNWDPWGQGT	126
b	121	LVTWSS	126

Db 132 GISSWYDYYGMDVWGQGTTVTVSS 155

RESULT 10
31696
g heavy chain v region - human (fragment)
Species: Homo sapiens (man)
;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
;Accession: S31696
Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougerousse, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
;Description: Mechanisms that generate human immunoglobulin diversity operate from the

;Accession: S31696
;Status: Preliminary
;Molecule type: mRNA
;Residues: 1-139 <CUT>
;Cross-references: EMBL:Z14194; NID:g30975; PRID:CAA78563.1; PID:g30976
;Superfamily: immunoglobulin V region; immunoglobulin homology
;Keywords: heterotrimer; immunoglobulin
;34-116/Domain: immunoglobulin homology <IMM>

Query Match	Score	DB	Length
Best Local Similarity	76.3%	570.5	139
Matches	81.5%	DB 2;	
110; Conservative	Pred. No. 2.2e-44;		
5; Mismatches	18;		
10; Indels	1;		
1; Gaps			
1 MKHLWLFULLVVAAPRWLISQVQLQOWAGGLKQSETSLTCAVYGGSPRSGYWSWIROPP	60		
1 MKHLWLFULLVVAAPRWLISQVQLQESPGCLVKRPSETSLTCAVYGGSSISYYWSWIROPA	60		
61 GKGLEWICBINFHGSTNTNPLSRSVTISVUDSKNOKSILKLSVTAADTAVYCAR-EIA	119		
61 AKGLEWIGRITSTGSTNTNPLSKSRVIMSVDISKNOFSILKLSVTAADTAVYCARGGLG	120		
120 ARPHRYFDWGOETL 134			
121 LTGDKWIDWGGQTL 135			

ESULT 11
31511
g heavy chain - human
;species: Homo sapiens (man)
;date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
;accession: S31511
;Chastagner, P.; Demaison, C.; These, J.; Zouali, M.
;submitted to the EMBL Data Library, December 1992
;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto

;Accession: S31511
;Name: heterorecombinant immunoglobulin V region
;Status: Preliminary
;Molecule type: mRNA
;Residues: 1-155 <CHA>
;Cross References: EMBL:X69865; NID:93394; PID:CAA49500.1; PID:933095
;superfamily: immunoglobulin V region; immunoglobulin homology
;Keywords: heterorecombinant; immunoglobulin

EQUITY IN THE 1990S: THE UNITED STATES

Query Match 76.1%; Score 569.5; DB 2; Length 155;
 Best Local Similarity 77.8%; Pred. NO. 3.1e-4;

Db 132 GISSWYDYYGMDVWGQGTTVTVSS 155

```

RESULT 12
S31512
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Accession: S31512
R:Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
C:Keywords: heterotrimer; immunoglobulin
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Domain: immunoglobulin homology <IMM>
A;Accession: S31512
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-155 <CHA>
A;Cross-references: EMBL:X69860; NID:933082; PIDN:CAA49494;1;
F:47-129

```

RESULT 13
S09711 Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C:Accession: S09711
R:Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Bloch, J. 268, 135-140, 1990

A;Title: Nucleotide sequences and three-dimensional modelling of the reference number: S99710, MURID:9262535
A;Accession: S09711
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-146 <HUG>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin

F;34-118/Domain: immunoglobulin homology <IMM>

C;Keywords: heterotetramer; immunoglobulin homology <IMM>

Query Match 74.9%; Score 560.5; DB 2; Length 146;

Best Local Similarity 76.0%; Pred. No. 1.9e-43; Matches 111; Conservative 8; Mismatches 20; Indels 7; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Search completed: March 9, 2001, 16:44:01

Job time: 60 sec

F;15-97/Domain: immunoglobulin homology <IMM>

C;Keywords: heterotetramer; immunoglobulin homology <IMM>

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

Query Match 74.1%; Score 554.5; DB 2; Length 143;

Best Local Similarity 86.0%; Pred. No. 6.3e-43; Matches 111; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

RESULT 14

B23746

Ig Fab region IV-J(H4)-C (KAU cold agglutinin) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000

C;Accession: B23746

R;Leoni, J.; Ghiso, J.; Frangione, B.

J;Biol. Chem. 266, 2836-2842, 1991.

A;Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunog

A;Reference number: A23746; MUID:1113155

A;Status: Preliminary

A;Residues: 1-231 <LEO>

C;Superfamily: immunoglobulin C region; immunoglobulin homology <IMM>

F;146-209/Domain: immunoglobulin homology <IMM>

RESULT 15

B49058

Ig heavy chain V-IV region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999

C;Accession: B49028

R;Timmers, E.; Kenter, M.; Thompson, A.; Krakman, M.E.; Berman, J.E.; Alt, F.W.; Schuur

Eur. J. Immunol. 21, 2355-2363, 1991

A;Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphot

A;Reference number: A49028; MUID:92008140

A;Accession: B49028

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-143 <TIM>

A;Cross-references: GB:664473; NID:9236906; PIDN:AAB20012.1; PID:9236907

A;Experimental source: X-linked agammaglobulinemia patients, B lymphoblastoid cell lines

A;Note: sequence extracted from NCBI backbone (NCB:64473, NCBI:64472)

C;Superfamily: immunoglobulin V region; immunoglobulin homology

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG HEAVY CHAIN V-II REGION WAH.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]

RP SEQUENCE.

RX MEDLINE=82222235; PubMed=6806818;

RA Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;

RT "Complete amino acid sequence of the delta heavy chain of human immunoglobulin D.";

RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).

CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA PROTEIN.

DR PIR: A02099; D2H0WA.

DR HSSP: P01825; 7EAB.

DR INTERPRO: IPR003006; -.

DR PFAM: PF00047; 19; 1.

KW Immunoglobulin V region.

FT SEQUENCE 129 AA; 14117 MW; D5D3D47ABE51319 CRC64;

Query Match 55.0%: Score 411.5; DB 1; Length 129; Best Local Similarity 62.1%; Pred. No. 1; 4e-32; Matches 82; Conservative 14; Mismatches 21; Indels 15; Gaps 3;

QY 20 OYQDQWAGGLKPKSEPLSLLTCAVIGGSF--SGYKMSWIRROPGKLEWIGEINHSGSTN 77

Db 1 RQQLQSGPGLVKPSEPLSLLTCAVIGGSF--SGYKMSWIRROPGKLEWIGEINHSGSTN 77

QY 78 YNPSLKSRSVTISVDTSKNQFSKIKLSSVTAADTAVVYCAREIAARPHRF-----D 127

Db 61 YNPSLKSRSVTISVDTSKNQFSKIKLSSVTAADTAVVYCAREIAARPHRF-----D 117

QY 128 YWGQGTLYTVSS 139

Db 118 VWGQGTLYTVHVS 129

RESULT 3

HV46_MOUSE STANDARD; PRT; 137 AA.

ID HV46_MOUSE

AC P01822;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG HEAVY CHAIN V REGION MOPC 315 PRECURSOR.

OS Mus musculus (Mouse);

OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RN [1]

RP SEQUENCE FROM N A.

RX MEDLINE=82238351; PubMed=2497341;

RA Rintfret A., Horne C., Dorrington K.J., Klein M.;

RT "Cloning, sequencing and expression of the rearranged MOPC 315 VH gene segment.", Mol. Immunol. 26:431-434(1989).

RL 12]

RP SEQUENCE OF 1-31.

RX MEDLINE=78094475; PubMed=414225;

RA Jilka R.L., Peskola S.;

RT "Amino acid sequence of the precursor region of MOPC-315 mouse immunoglobulin heavy chain.", Proc. Natl. Acad. Sci. U.S.A. 74:5692-5695(1977).

RN [3]

RP SEQUENCE OF 1-21.

RX MEDLINE=79148758; PubMed=428562;

RA Schechter I., Wolf C., Zemel R., Burstein Y.;

RT "Structure and function of immunoglobulin genes and precursors.", Fed. Proc. 38:1839-1845(1979).

RN [4]

RP SEQUENCE OF 19-136.

Query Match 54.5%: Score 408; DB 1; Length 137; Best Local Similarity 60.3%; Pred. No. 3; 3e-32; Matches 85; Conservative 18; Mismatches 32; Indels 6; Gaps 4;

QY 1 MKHLWFLPLLYAIPRVLWSQVOLQWAGGLKPKSEPLSLLTCAVIGGSF--SGYKMSWIRQ 59

Db 1 MKVLSLYLILTAIP-GIMSDVQLOESGPGVGLKPKSEPLSLLTCAVIGGSF--SGYKMSWIRQ 59

QY 60 PGKGLWIGETNHSGSTNQFSKIKLSSVTAADTAVVYCAREIA 119

Db 60 PGKNLWLGFTKYGDSNGYNPSLKNRVSITRDTSENQFELKLNSTTDTATYCAGD-- 117

QY 120 ARPH-RYFDYQGQTVTVSS 139

Db 118 -NDHLYFDFWQGQTVTVSS 137

RESULT 4

HV2G_HUMAN STANDARD; PRT; 117 AA.

ID HV2G_HUMAN

AC P01825;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1985 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG HEAVY CHAIN V-II REGION NERM.

RX MEDLINE=74170779; PubMed=524622;

RA Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.;

RT "Amino-acid sequence of the variable region of the heavy (alpha) chain of a mouse myeloma protein with anti-hapten activity.", Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).

RN [5]

RP REVISION TO 53.

RX MEDLINE=77444979; PubMed=268248;

RA Hood L., Margolies M.N., Givol D., Zakut R.;

RT Unpublished results, cited by:

RL Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;

RL Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).

CC -1- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.

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CC

DR EMBL: M27638; CAA61317.1; -;

DR EMBL: X07880; CAA30727.1; -;

DR PIR: P10102; AVMS35.

DR INTERPRO: IPR003006; -.

DR PFAM: PF00047; 19; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 18

FT CHAIN 19 137

FT DOMAIN 19 48

FT DOMAIN 49 54

FT DOMAIN 55 68

FT DOMAIN 69 84

FT DOMAIN 85 116

FT DOMAIN 117 126

FT DOMAIN 127 137

FT DISULFID 40 114

FT CONFLICT 15 15

FT CONFLICT 15 15

FT CONFLICT 77 78

FT CONFLICT 102 102

FT CONFLICT 123 123

FT CONFLICT 137 137

FT NON_TER 137 AA; 15399 MW; FB3B28304C2B81DC CRC64;

Query Match 54.5%: Score 408; DB 1; Length 137; Best Local Similarity 60.3%; Pred. No. 3; 3e-32; Matches 85; Conservative 18; Mismatches 32; Indels 6; Gaps 4;

QY 1 MKHLWFLPLLYAIPRVLWSQVOLQWAGGLKPKSEPLSLLTCAVIGGSF--SGYKMSWIRQ 59

Db 1 MKVLSLYLILTAIP-GIMSDVQLOESGPGVGLKPKSEPLSLLTCAVIGGSF--SGYKMSWIRQ 59

QY 60 PGKGLWIGETNHSGSTNQFSKIKLSSVTAADTAVVYCAREIA 119

Db 60 PGKNLWLGFTKYGDSNGYNPSLKNRVSITRDTSENQFELKLNSTTDTATYCAGD-- 117

OS Homo sapiens (Human); Chordata; Craniata; Vertebrata; Euteleostomi; RC
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; RC
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. RX
 RN [1] SEQUENCE. RA
 RP MEDLINE=77242302; PubMed=407927; RA
 RX RA
 RA Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.; RA
 RT "Amino acid sequence of the VH region of a human myeloma RA
 immunoglobulin (IgG New)."; RA
 RL Biochemistry 16:3412-3420(1977). RL
 RN [2] X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT. RN
 RP MEDLINE=78066916; PubMed=618887; RP
 RA Saul F.A., Amzel L.M., Poljak R.J.; RA
 RT "Preliminary refinement and structural analysis of the Fab fragment RA
 from human immunoglobulin new at 2.0-A resolution.>"; RT
 RL J. Biol. Chem. 253:585-597(1978). RL
 CC [1] -I- MISCCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IgG1 MYELOMA CC
 PROTEIN. DR
 DR PIR; A02100; G1HNM. DR
 DR PDB; 7FAB; 31-JAN-94. DR
 DR INTERPRO; IPR003006; -. DR
 DR PFAM; PF00047; Ig; 1. DR
 DR PPNM; PF00047; Ig; 1. DR
 KW IMMUNOGLOBULIN V REGION; SIGNAL. KW
 KW IMMUNOGLOBULIN V REGION; 3D-STRUCTURE. KW
 KW PYRROLIDONE CARBOXYLIC ACID. KW
 MOD_RES 1 1
 FT STRAND 3 7
 FT STRAND 11 12
 FT TURN 14 15
 FT STRAND 18 25
 FT TURN 30 31
 FT STRAND 33 39
 FT TURN 41 42
 FT STRAND 46 51
 FT TURN 53 54
 FT STRAND 57 59
 FT HELIX 61 63
 FT TURN 64 66
 FT STRAND 67 72
 FT TURN 73 76
 FT STRAND 77 82
 FT HELIX 87 89
 FT STRAND 91 98
 FT STRAND 104 107
 FT STRAND 111 115
 FT NON_TER 117 117
 SQ 117 AA; 12790 MW; 2DA47B509562D237 CRC64;

Query Match 53.1%; Score 397.5; DB 1; Length 117; RESULT 6
 Best Local Similarity 64.1%; Pred. No. 1; 1e-28; HV43_MOUSE
 Matches 75; Conservative 15; Mismatches 25; Indels 2; Gaps 2; RT
 ID HV43_MOUSE STANDARD; PRT; 144 AA. RT
 AC P01819; RT
 DT 21-JUL-1986 (Rel. 01; Created) RT
 DT 21-JUL-1986 (Rel. 01; Last sequence update) RT
 Db 1 MKHLWFLFLVAAPRWLQLSQVQLQDQAGLILKPKSETLISLTCAYVGGF-SYYWWSIROP 59 RT
 QY 60 PSKGLEMEIGENHSGSTNYNPNSLKSRTVTISVTSKNSFLKLSVTAADTAVYCAR 116 RT
 DE 60 PGNKLEMNGYTSYDGSNNNPNSLKRISITDTSKNOFLKNSVTTEDTATYCAR 116 RT
 OS IG HEAVY CHAIN V REGION MOPC 141 PRECURSOR. OS
 OC MUS musculus (Mouse). OC
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. OC
 RN [1] SEQUENCE FROM N.A. RN
 RP SEQUENCE FROM N.A. RP
 RX MEDLINE=81012133; PubMed=5774258; RX
 RA Sakano H., Maki R., Kuroso Y., Roeder W., Tonegawa S.: RA
 RT "Two types of somatic recombination are necessary for the generation RT
 of complete immunoglobulin heavy-chain genes.>"; RT
 RL Nature 286:676-683 (1980). RL
 CC -I- MISCCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A CC
 CC DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IgG2B. CC
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 DR EMBL; J00491; AAA38121.1; DR
 DR EMBL; V00768; CAA2149.1; -. DR
 DR PIR; A02094; G20514. DR
 DR INTERPRO; IPR003006; -. DR
 DR PFAM; PF00047; Ig; 1. DR
 DR KW IMMUNOGLOBULIN V REGION; SIGNAL. KW
 FT CHAIN 1 19 FT
 CHAIN 20 144 FT
 IG HEAVY CHAIN V REGION MOPC 141. FT

Qy	8	LLVAAPRWLSQVQDQWQAGLKPSETSLTCAVGGFSGYWMSWIRQPGKLEWI 67	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Murida; Murinae; Mus. RN [1]
Db	8	LFLAATPATGVQPGSLKSCASGFDPSRYWMWRQPGKLEWI 67	RN RP SEQUENCE FROM N. A.
Qy	68	GEIN HSGSTNWPNSLKSRSVTSVDTSKNQFLSSVTAADTAVYCARRIARPHRF 126	RA STRAIN=BALB/CJ; PubMed=2499654; RX MEDLINE=89279143; PIR; JG: 169; 2007-2019(1989).
Db	68	GRIDPNSSGTTYNEHRSKATLTIKPSSTAYMQLSLSDSAVYCAR--YRLGRYF 124	RA "Early onset of somatic mutation in immunoglobulin VH genes during the primary immune response." RT J. Exp. Med. 169; 2007-2019(1989).
Qy	127	DYWGQQLTVSS 139	RL DR PIR; JG: 0510; HWS73.
Db	125	DYWGQQLTVSS 137	DR INTERPRO; IPR003006; -.
RESULT	12		DR PFAM; PF00047; 1g; 1.
HV37_MOUSE		HV37_MOUSE STANDARD; PRT; 119 AA.	KW Immunoglobulin V region; Signal.
ID		AC P01807;	FT SIGNAL 1 18
DT		DT 21-JUL-1986 (Rel. 01, Created)	FT CHAIN 19 117
DT		DT 21-JUL-1986 (Rel. 01, Last sequence update)	FT DISULID 40 115
DE		DE IG HEAVY CHAIN V REGION X4.	FT NON_TER 117 117
OS		OS Mus musculus (Mouse)	SO SEQUENCE 117 AA; 13223 MW; 1595517827F976BE CRC64;
OC		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Murida; Murinae; Mus. [1]	
RP		RP SEQUENCE.	
RX		RX MEDLINE=79223895; PubMed=111245;	
RA		RA Rao D.N., Rudikoff S., Krutzsch H., Potter M.;	
RT		RT "Structural evidence for independent joining region gene in immunoglobulin heavy chains from anti-galactan myeloma proteins and its potential role in generating diversity in complementarity-determining regions";	
RT		RT Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).	
RL		RL -.- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN THAT BINDS GALACTAN.	
CC		CC PIR; A02077; AVMSX4.	
DR		DR HSSP; P01810; 2FBJ.	
DR		DR INTERPRO; IPR003006; -.	
DR		DR PFAM; PF00047; 1g; 1.	
KW		KW Immunoglobulin V region.	
FT		FT NON_TER 119 119	
SEQUENCE		SEQUENCE 119 AA; 13246 MW; BC34FC8F31CD41B3 CRC64;	
RESULT	14		
HV38_MOUSE		HV38_MOUSE STANDARD; PRT; 119 AA.	
ID		AC P01808;	
DT		DT 21-JUL-1986 (Rel. 01, Created)	
DT		DT 21-JUL-1986 (Rel. 01, Last sequence update)	
DE		DE IG HEAVY CHAIN V REGION 1601.	
OS		OS Mus musculus (Mouse)	
OC		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Murida; Murinae; Mus. [1]	
RP		RP SEQUENCE.	
RX		RX MEDLINE=79223895; PubMed=111245;	
RA		RA Rao D.N., Rudikoff S., Krutzsch H., Potter M.;	
RT		RT "Structural evidence for independent joining region gene in immunoglobulin heavy chains from anti-galactan myeloma proteins and its potential role in generating diversity in complementarity-determining regions";	
RT		RT Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).	
CC		CC -.- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN THAT BINDS GALACTAN.	
CC		CC PIR; A02078; AVMS76.	
DR		DR HSSP; P01810; 2FBJ.	
DR		DR INTERPRO; IPR003006; -.	
DR		DR PFAM; PF00047; 1g; 1.	
KW		KW Immunoglobulin V region.	
FT		FT NON_TER 119 119	
SEQUENCE		SEQUENCE 119 AA; 13169 MW; BC38CC84E6EA00E8 CRC64;	
RESULT	13		
HV62_MOUSE		HV62_MOUSE STANDARD; PRT; 117 AA.	
ID		AC HV62_MOUSE STANDARD; PRT; 117 AA.	
AC		AC P08533;	
DT		DT 01-NOV-1990 (Rel. 16, Created)	
DT		DT 01-NOV-1990 (Rel. 16, Last sequence update)	
DT		DT 15-JUL-1999 (Rel. 38, Last annotation update)	
DE		DE IG HEAVY CHAIN V REGION 733 PRECURSOR.	
OS		OS Mus musculus (Mouse).	

RESULT	15
Qy	79 NPSLSKRSVTVSDTTSKNOFSKLSSTAAADPAAVYCAELARAPHRPHFDYNGQGTLYTVS 138
Db	61 TPSLKDKFISRDNAKNTLYLQMSKVRSEDTALYCCAR--LGYYGFDWNGAGTTVVS 117
Qy	139 S 139
Db	118 S 118

QY	79	NPLSKSRVTISVDTSKNQFSKILSSVTAADTAVYVCAREIAARPHRYFDWQGQTLVTVS	138
		: - : : : : : : : :	
Db	61	TPSLKDKFILSRDNARNLNLQMSKVRSEDALYICAR--LHYVGYNAWQGQTLVTVS	117
QY	139	S 139	
Db	118	A 118	

ID	HV40_MOUSE	STANDARD;	PRT;	119 AA.
AC	P01830;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	IG HEAVY CHAIN V REGION J539.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
RN	[1]			
RP	PRELIMINARY SEQUENCE.			
RX	MEDLINE=9223855; Pubmed=111245;			
RX	Rao D. N., Rudikoff S., Krutzsch H., Potter M.;			
RX	Rudikoff S., Krutzsch H., Potter M., Rao D. N.,			
RX	"Structural evidence for independent joining region gene in immunoglobulin heavy chains from anti-galactan myeloma proteins and its potential role in generating diversity in complementarity-determining regions.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 76:2090-2094 (1979).			
RN	[2]			
RX	X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).			
RX	MEDLINE=88217652; Pubmed=3449853;			
RA	Suh S. W., Bhat T. N., Navia M. A., Cohen G. H., Rao D. N., Rudikoff S.,			
RA	Davies D. R.;			
RT	"The galactan-binding immunoglobulin Fab J539: an X-ray diffraction study at 2.6-A resolution.";			
RT	Proteins 1:74-80 (1996).			
RL	-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS GALACTAN.			
CC	PIR: A02080; AVMSJ5.			
DR	PDB: 2FB1, 15-OCT-90.			
DR	INTERPRO; IPR003006; -.			
DR	PFAM; PF00047; Ig; 1.			
KW	Immunoglobulin V region; 3D-structure.			
FT	NON_TER 119 119			
FT	STRAND 3 7			
FT	STRAND 10 12			
FT	TURN 14 15			
FT	STRAND 18 25			
FT	HELIX 29 31			
FT	STRAND 34 39			
FT	TURN 41 42			
FT	STRAND 45 51			
FT	TURN 53 54			
FT	STRAND 58 60			
FT	TURN 62 67			
FT	STRAND 68 72			
FT	STRAND 78 83			
FT	HELIX 88 90			
FT	STRAND 92 100			
FT	TURN 101 103			
FT	STRAND 104 108			
FT	STRAND 112 116			
SEQUENCE	119_AA; 13240 MW; 577B4F1DB675C1F1 CRC64;			

Query Match 43.4%; Score 325; DB 1; Length 119;
 Best Local Similarity 53.7%; Pred. No. 2; $2\text{-}e^{-24}$
 Matches 65; Conservative 19; Mismatches 33; Indels 4; Gaps 2

Fri Mar 9 16:49:08 2001

us-09-203-768a-2.rsp

GenCore version 4.5
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OM protein - protein search, using sw model

Run on:

March 9, 2001, 16:43:41 ; Search time 38.3 Seconds

(without alignments)
425.376 Million cell updates/sec

Title: US-09-203-768a-2

Perfect score: 748

Sequence: 1 MKHLWFFLLVAAAPRWLSQL... ARPHRYFDIYWGOGTLWVSS 139

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_15:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rabbit:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_unlabeled:
16: sp_unpublished:
17: sp_unreviewed:
18: sp_unsubmittable:
19: sp_untranslated:
20: sp_worm:
21: sp_yeast:
22: sp_zebrafish:
23: sp_chicken:
24: sp_fly:
25: sp_mouse:
26: sp_rat:
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DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)
 DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 GN VH.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 NCBI_TaxID=9606;
 [1]
 RP TISSUE=INTESTINE;
 RC SEQUENCE FROM N.A.
 RA Fischer M.; Klüppers R.;
 RT "Human IgA and IgM secreting intestinal plasma cells carry heavily
 mutated VH region genes";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ009522; CA008729; 1; -.
 DR INTERPRO: IPR03006; -.
 DR PFAM: PF00047; 1g; 1.
 FT NON_TER 1 1
 FT NON_TER 82 82
 SQ SEQUENCE 82 AA; 9566 MW; 4325325C6570987A CRC64;

RESULT 6
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 ID Q9UL84 PRELIMINARY; PRT; 122 AA.
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 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
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 RP SEQUENCE FROM N.A.
 RX MEDLINE=8277139; PubMed=9614934;
 RA Wu X.; Liu B.; Van der Merwe P.L.; Kalis N.N.; Berney S.M.;
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR Q9UL84; AAD56254; 1; -.
 DR INTERPRO: IPR03006; -.
 DR PFAM: PF00047; 1g; 1.
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 SQ SEQUENCE 121 AA; 13695 MW; D582D450596BDD35 CRC64;

RESULT 6
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 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
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 RA Wu X.; Liu B.; Van der Merwe P.L.; Kalis N.N.; Berney S.M.;
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
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 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL: AF0335030; AAD56266; 1; -.
 DR HSSP: P01772; 2FB4; -.
 DR INTERPRO: IPR03006; -.
 DR PFAM: PF00047; 1g; 1.
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Query Match 42.0%; Score 314; DB 4; Length 122;
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 Matches 63; Conservative 19; Mismatches 38; Indels 2; Gaps 2;

RESULT 8
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 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
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 RP SEQUENCE FROM N.A.
 RA Clemens A.; Rademakers A.; Specht C.; Koelsch E.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ225171; CAB65236; 1; -.
 DR INTERPRO: IPR03006; -.
 DR PFAM: PF00047; 1g; 1.

Query Match 79.0%; Score 790; DB 4; Length 137;
 best Local Similarity 79.0%; PRED. NO. 9.3e-25;
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RESULT 7
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 ID Q9UL96 PRELIMINARY; PRT; 121 AA.
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 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
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 RP SEQUENCE FROM N.A.
 RX MEDLINE=8277139; PubMed=9614934;
 RA Wu X.; Liu B.; Van der Merwe P.L.; Kalis N.N.; Berney S.M.;
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
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 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR Q9UL96; AAD56254; 1; -.
 DR INTERPRO: IPR03006; -.
 DR PFAM: PF00047; 1g; 1.
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 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
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 RX MEDLINE=8277139; PubMed=9614934;
 RA Wu X.; Liu B.; Van der Merwe P.L.; Kalis N.N.; Berney S.M.;
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR Q9UL96; AAD56254; 1; -.
 DR INTERPRO: IPR03006; -.
 DR PFAM: PF00047; 1g; 1.
 FT NON_TER 1 1
 FT NON_TER 121 121
 SQ SEQUENCE 121 AA; 13695 MW; D582D450596BDD35 CRC64;

DE VH3 PROTEIN (FRAGMENT).
 GN VH3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TAXID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95071149; PUBMED=7475288;
 RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
 LICHTENSTEIN A.R., BERENSON J.R.;
 RT "A CD10-positive subset of malignant cells is identified in multiple
 myeloma using PCR with patient-specific immunoglobulin gene primers.",
 RL Leukemia 9:1948-1953(1995).
 EMBL: S80800; AAD14139.1; -.
 DR HSSP: P01722; 2FB4.
 DR INTERPRO: IPR003006; -.
 DR PFAM: PF00047; 1g; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 147 AA; 15768 MW; 8489FCAA7BC925C CRC64;

Query Match 40.6%; Score 304; DB 4; Length 147;
 Best Local Similarity 48.1%; Pred. No. 1.2e-23; Gaps 3;
 Matches 63; Conservative 20; Mismatches 32; Indels 16;
 Gaps 3;
 Qy 20 QVQLOQWAGGLIKPRTTLSLTCAVYGGFSFGYYWWIRQPPGKGHLIEWIGEINHSSTNYN 79
 Db 1 QVHLVESGGVVQPSKSLRLSCEASGFTFSTYGMSSWRQAPGKGLDWVALISYDSTQYR 60
 Qy 80 P-SLRSRVTSVDTKNSFLKLSVTAATAVVYCARETAAPRPHRYF-----DY 128
 Db 61 AGSVVGRFTISRDNSKNTLYLQMTSLRVEDIAVYCAKD----GNYFDSVGVYYAGIDY 115
 Qy 129 WGQGFLTVSS 139
 Db 116 WGQGFLTVSS 126

Search completed: March 9, 2001, 16:46:47
 Job time: 186 sec

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Gencore version 4.5

OM protein - protein search, using sw model

Run on: March 9, 2001, 16:43:34 ; Search time 26.57 Seconds

(without alignments)

150.571 Million cell updates/sec

Title: US-09-203-768a-4

Perfect score: 615

Sequence: 1 LMLPDTTGERVMTQSPATL... QYNNWPPYTFGQGTLEIKR 117

Scoring table: BL0SUM62 Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_36:*

1: /SIDS1/gcdata/geneseq/geneseq/AA1980.DAT:*

2: /SIDS1/gcdata/geneseq/geneseq/AA1981.DAT:*

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4: /SIDS1/gcdata/geneseq/geneseq/AA1984.DAT:*

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14: /SIDS1/gcdata/geneseq/geneseq/AA1994.DAT:*

15: /SIDS1/gcdata/geneseq/geneseq/AA1995.DAT:*

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17: /SIDS1/gcdata/geneseq/geneseq/AA1997.DAT:*

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20: /SIDS1/gcdata/geneseq/geneseq/AA2000.DAT:*

21: /SIDS1/gcdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score % Query Match Length DB ID

Description

ALIGNMENTS

RESULT	1
R52951	ID R52951 standard; Protein; 234 AA.
XX	XX
AC R52951;	AC
XX	XX
DR 27-OCT-1994 (first entry)	DR
XX	XX
DE Human anti-IgE Mab light chain.	DE
XX	XX
KW Human IgE; C4 region; triggers mediator release; Mast cells; Monoclonal antibody; allergy.	KW
XX	XX
OS Homo sapiens.	OS
XX	XX
FH Key	Location/Qualifiers
FT Region	21..128 /label= light chain variable region
FT	
XX	
PN EP592230-A.	PN
XX	XX
PD 13-APR-1994.	PD
XX	XX
PF 07-OCT-1993; 93EP-0308006.	PF
XX	XX
PR 07-OCT-1992; 92EP-029380.	PR
XX	XX
PA (SNOW) SNOW BRAND MILK PROD CO LTD.	PA
XX	XX
PI Goto M, Kobayashi F, Mizuno A, Morinaga T, Washida N;	PI
PT Yoshioka T;	PT
XX	XX
DR WPI: 1994-120330/15.	DR
DR N-PSDB; Q71872.	DR
XX	XX

F105 rearranged va
F105VK-F105K. Ho
Human monoclonal Ho
ORF 1 of IgG light
Human IgG light chain
Human ScFv light c
Human V-kappa frag
Human V-kappa vK65
Human v kappa subg
Human DNA vKappa65
Anti-human TNF-alpha
Immunoglobulin r10
DNA fragment vK65.
Light Chain variab
Light chain variab
Mouse anti-nerotox
Anti-P. aeruginosa
Light chain variab
Light chain variab
Human V-kappa frag
Human V-kappa vK65
DNA fragment vK65.
Human vKappa65.5 f
Human DNA vKappa55
Amino acid sequenc
Human V-kappa frag
Human V-kappa vK65
DNA fragment vK65.

Query	Match	85.9%	Score	528.5	DB	20	Length	213
Best	Local Similarity	91.8%	Pred. No.	7.7e-32				
Matches	101;	Conservative	6;	Mismatches	2;	Indels	1;	Gaps
Oy	9	EIVMTOOSPATLVSVPGERATLSCRASOVSSNLAWIQOKPGQAPRLIYGASTRANGIPA	68					
Db	1	eleltqspatlsvsperatlscreasvsdlaqwqgkpgapriliygastralgypa	60					
Oy	69	RFGSGSGTERMLTISLQSDFAWVYQQINNNWPP-YTFCGOTKIEIKR	117					
Db	61	rfsgsqaafiltisslasedfavyvcoqgnwnppytfcgatleikr	110					

Query Match 85.0%; Score 523; DB 14; Length 129;
 Best Local Similarity 87.3%; Pred. No. 1.2e-31; Mismatches 6; Indels 2; Gaps 2;
 Matches 103; Conservative 7; Mismatches 6; Indels 2; Gaps 2;

QY 1 LWLPLPTGETVMTQSSPATSVSPGRATSGCRASQSSN-LAWYQOKGQAPRLLIYGA 59
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 13 1wlpttgeivltqsgptlspgeratiscrasqssvssylawqkbgaprtliya 72

QY 60 STRATGIPARFSGSGTETLTISLQSEDFAVYICQQYNNWPPYTFGGTKEIKR 117
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 :|||||:|||||:|||||:|||||:|||||:|||||:
 Db 73 ssratgiparftsgsgtqdfltltisrlpedfavyycqygs-spytfqggtkleikr 129

RESULT 6
 W47582 standard; Protein; 117 AA.
 XX
 AC W47582;
 XX
 DT 22-JUN-1998 (first entry)
 DE Human monoclonal antibody light chain variable region.
 XX
 KW Human; monoclonal antibody; hybridoma cell strain TTG6; hmab;
 XX
 antitetanus toxin.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 24..34
 FT /label= CDR1
 FT 49..55
 FT /label= CDR2
 FT Region 89..98
 FT /label= CDR3
 XX
 JP10014570-A.
 XX
 PD 20-JAN-1998.
 XX
 PP 05-JUL-1996; 96JP-0194095.
 PR 05-JUL-1996; 96JP-0194095.
 XX
 PA (MATS/) MATSUDA M.
 PA (MOMI) MORINAGA & CO LTD.
 XX
 DR WPI: 1998-138233/13.
 DR N-PSDB; V18674.
 XX
 PT New cDNA encoding human monoclonal antibody - useful for production
 PT of antibody by hybridoma techniques commercially
 XX
 PS Claim 4; Fig 2; 8pp; Japanese.

CC The present sequence represents a human monoclonal antibody (hmab) light chain variable region. The cDNA encoding the hmab can be used for commercial production of the hmab. The cDNA was isolated from an antitetanus toxin human monoclonal antibody producing hybridoma cell strain TTG6. Sequence 117 AA;

Query Match 84.2%; Score 518; DB 19; Length 117;
 Best Local Similarity 90.8%; Pred. No. 2.6e-31; Mismatches 4; Indels 0; Gaps 0;
 Matches 99; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 9 EIVMTQSPATLSVFFGERATLSCRASQSSN-LAWYQOKGQAPRLLIYGA 68
 :|||||:|||||:|||||:|||||:|||||:|||||:
 1..divmtqspatlsvffgeratlsrasqssvqtnlawyqqkpgqaprtliya 60

Db

RESULT 7
 DE R12128 standard; Protein; 349 AA.
 XX
 AC R12128;
 XX
 DT 01-AUG-1991 (first entry)
 DE 1B1 IgG aberrant light chain with duplicated variable region.
 XX
 KW immunoglobulin G; light chain; variable region; duplication;
 KW passive immunity; group B streptococci.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..17
 FT /label= leader peptide
 FT Region 18..130
 FT /label= variable region
 FT /note= "L' V 1"
 FT Region 131..243
 FT /label= variable region
 FT /note= "L' V 2"
 FT Region 244..345
 FT /label= constant region
 XX
 PN W09106305-A.
 XX
 PD 16-MAY-1991.
 XX
 PP 06-NOV-1990; 90WO-US06426.
 XX
 PR 07-NOV-1989; 89US-0432700.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIB.
 XX
 PT Shuford WW, Harris LJ, Raff HV;
 XX
 DR WPI: 1991-163947/22.
 DR N-PSDB; Q11878.

XX
 PT Oligomeric immunoglobulin(s) with high avidity for antigen(s) -
 PT formed by duplicating esp. variable region of light chain of IgG
 PT class
 XX
 PS Example 5; Fig 16; 104pp; English.
 XX
 CC This sequence is deduced from the cDNA clone 4B9-vk15 and includes the amino acid sequence beyond the first stop codon. The clone is incomplete, starting from the G of the ARG initiator codon, but the initial Met is given. Antibody molecules of the invention can include one or two aberrant light chains containing a duplicated variable region, to produce heavier antibodies. These heavier antibodies were found to have higher avidity than antibodies with just a single copy of the L'V region. The antibodies can be used to treat disease, e.g. infection by Streptococcus agalactiae. They are able to pass across the placenta.
 CC See also Q11879 and Q11880.
 XX
 SQ Sequence 349 AA;

Query Match 83.5%; Score 513.5; DB 12; Length 349;
 Best Local Similarity 85.5%; Pred. No. 1.5e-30; Mismatches 10; Indels 1; Gaps 1;
 Matches 100; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 IWLDPDTGEIWTQSPATLSVSPGERATLSGRASSVSSNLAWYQOKPGAPRLIYGAS 60
 Db 13 Iwlpdttgeiwtqspatlsvgeratlsrasqsvsylawyqkpgaprpiliyas 72
 QY 61 TRATGIPARFSGSGSGSTEFTIISQEDDAVYCCQYNNWPP-YTFGQCTKLEIK 116
 Db 73 nratgiparfsgsgsgtdftltisslepedfavyycqhrdnwppatfgggtkeik 129
 RESULT 8 R13111 standard; Protein; 414 AA.
 ID R13111 standard; Protein; 414 AA.
 XX R13111;
 AC R13018
 XX 01-AUG-1991 (first entry)
 DE 1B1 IgG aberrant light chain with duplicated variable region.
 XX KW immunoglobulin G; light chain; variable region; duplication;
 XX passive immunity; group B streptococci.
 OS Homo sapiens.
 XX
 FH Key
 FT peptide
 FT Region
 FT /label= leader peptide
 FT 18..130
 FT /label= variable region
 FT /note= "L'V 1"
 FT 131..243
 FT /label= variable region
 FT /note= "L'V 2"
 FT 244..345
 FT /label= constant region
 PN WO9106305.A.
 PD 16-MAY-1991.
 XX 06-NOV-1990; 90WO-US06426.
 PA (BRIM) BRISTOL-MYERS SQUIB.
 XX
 PI Shuford WW, Harris LJ, Raff HV;
 XX DR WPI: 1991-163947/22.
 DR N-PSDB; Q11878.
 XX
 PT Oligomeric immunoglobulin(s) with high avidity for antigen(s) -
 PT formed by duplicating esp. variable region of light chain of IgG
 PT class
 XX
 PS Example 5; Fig 16; 104pp; English.

This sequence is deduced from the cDNA clone 4B9-VK15 and includes the amino acid sequence beyond the first stop codon ("x" in the sequence represents a nonsense codon). The clone is incomplete, starting from the G of the ATG initiator codon, but the initial Met is given. Antibody molecules of the invention can include one or two aberrant light chains containing a duplicated variable region, to produce heavier antibodies. These heavier antibodies were found to have higher avidity than antibodies with just a single copy of the L'V region. The antibodies can be used to treat disease, e.g. infection by Streptococcus agalactiae. They are able to pass across the placenta. See also Q11879 and Q11880.

Sequence 414 AA;

Query Match 83.5%; Score 513.5; DB 12; Length 414;
 Best Local Similarity 85.5%; Pred. No. 1; 8e-30;
 Matches 100; Conservative 6; Mismatches 10; Indels 1; Gaps 1;
 AC R13018
 XX 01-AUG-1991 (first entry) :
 DE 1B1 IgG aberrant light chain with duplicated variable region.
 XX KW immunoglobulin G; light chain; variable region; duplication;
 XX passive immunity; group B streptococci.
 OS Homo sapiens.
 XX
 FH Key
 FT peptide
 FT Region
 FT /label= leader peptide
 FT 18..130
 FT /label= variable region
 FT /note= "L'V 1"
 FT 131..243
 FT /label= variable region
 FT /note= "L'V 2"
 FT 244..345
 FT /label= constant region
 PN WO9106305.A.
 PD 16-MAY-1991.
 XX 06-NOV-1990; 90WO-US06426.
 PA (BRIM) BRISTOL-MYERS SQUIB.
 XX
 PI Shuford WW, Harris LJ, Raff HV;
 XX DR WPI: 1991-163947/22.
 DR N-PSDB; Q11878.
 XX
 PT Oligomeric immunoglobulin(s) with high avidity for antigen(s) -
 PT formed by duplicating esp. variable region of light chain of IgG
 PT class
 XX
 PS Example 5; Fig 16; 104pp; English.

This sequence is deduced from the cDNA clone 4B9-VK15 and includes the amino acid sequence beyond the first stop codon ("x" in the sequence represents a nonsense codon). The clone is incomplete, starting from the G of the ATG initiator codon, but the initial Met is given. Antibody molecules of the invention can include one or two aberrant light chains containing a duplicated variable region, to produce heavier antibodies. These heavier antibodies were found to have higher avidity than antibodies with just a single copy of the L'V region. The antibodies can be used to treat disease, e.g. infection by Streptococcus agalactiae. They are able to pass across the placenta. See also Q11879 and Q11880.

XX Anti-HBs monoclonal antibody - produced without the risk of Epstein
 PT Barr virus contamination
 XX Disclosure; Page 9-10; 12pp; Japanese.
 PS
 XX The invention relates to an anti-HBs monoclonal antibody having the
 following properties: (A) CDR-3 of H chain variable region; (B) it
 contains no Epstein Barr virus (EBV); (C) it binds at least one adr type
 among human HBs antigens. The anti-HBs monoclonal antibody is high in
 antibody titer and has low risk of EBV contamination. It can be used to
 prevent hepatitis C.
 XX
 SQ Sequence 214 AA;
 W1155 Query Match 82.8%; Score 509.5; DB 20; Length 214;
 Best Local Similarity 93.6%; Pred. No. 1.9e-30; Matches 102; Conservative 1; Mismatches 5; Indels 1; Gaps 1;
 AC Matches 102; Conservative 1; Mismatches 5; Indels 1; Gaps 1;
 XX
 AC W1155;
 XX
 AC 14-MAY-1997 (first entry)
 XX
 DE Anti-lung tumour antigen monoclonal antibody light chain.
 XX Light chain monoclonal antibody; antibody; TB2A36C3; lung; tumour; EBV;
 KW Epstein-Barr virus; TB945; human; B cell; screen; antigen;
 KW carcinoma; lysis; anti-tumour therapy; activation; CD4; CD8;
 KW cell.
 OS Homo sapiens.
 OS W09628473-A1.
 XX
 PD 19-SEP-1996.
 XX
 PF 18-MAR-1996; 96WO-US03661.
 XX
 PR 16-MAR-1995; 95US-0405034.
 XX
 PA (MED/+) MEDENICA R. D.
 XX
 PI Mukerjee S;
 XX
 WPI; 1996433764/43.
 DR N-PSDB; T33664.
 XX
 PT Anti-lung tumour antigen monoclonal antibody TB2A36C3 - produced by
 PT Epstein-Barr virus transformation of human lung cancer patient
 PT B-cells, useful in conjunction with other agents for lysis of
 PT tumours
 XX
 PS Claim 12; Page 25; 46pp; English.
 XX
 CC The present sequence is the light chain from the monoclonal
 antibody (Mab) TB2A36C3, which has high specificity against lung
 tumour antigens and is produced by an Epstein-Barr virus (EBV)
 transformed TB945 human B cell line. The Mab can be used to screen
 serum or tissue samples for a carcinoma associated antigen, lysis

CC tumours in anti-tumour therapy (optionally with other agents) and
 CC activate immune competent CD4 or CD8 cells in a patient's blood
 CC system.
 CC Tumour draining lymph nodes obtained from a non-SCLC (small cell
 CC lung cancer) patient were cut into fine pieces and mashed. Pure B
 CC cells isolated using CD19 coated immunomagnetic beads, were
 CC immortalised by EBV transformation, and plated and assayed for
 CC activity. Clones which showed positive reactivity with autologous
 CC tumour cells from the patient and the SCIC cell line NCIH9, were
 CC subjected to limiting dilution to prepare the Mab.
 XX
 SQ Sequence 134 AA;

W1155 Query Match 82.0%; Score 504.5; DB 17; Length 134;
 Best Local Similarity 84.7%; Pred. No. 2.8e-30; Matches 100; Conservative 5; Mismatches 12; Indels 1; Gaps 1;
 AC Matches 100; Conservative 5; Mismatches 12; Indels 1; Gaps 1;
 XX
 AC W1155;
 XX
 AC 01-NOV-1993 (first entry)
 XX
 DE F105 rearranged variable region light chain.
 XX Monoclonal antibody; MAb; envelope; glycoprotein; gp120; HIV; AIDS;
 KW CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
 KW chain; epitope; immune deficiency.
 OS Homo sapiens.
 XX
 FT Key Location/Qualifiers
 FT peptide 1..19
 FT /label= sig_peptide
 FT Protein 20..129
 FT /label= mat_protein
 XX
 PN W09312232-A.
 XX
 PD 24-JUN-1993.
 XX
 PF 10-DEC-1992; 92WO-US10928.
 XX
 PR 10-DEC-1991; 91US-0804652.
 XX
 PA (DAND) DANA FARBER CANCER INST INC.
 PA (NEWE-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
 XX
 PI Haseltine WA, Marasco WA, Posner MR, Sodroski JG;
 XX
 WPI; 1993-214174/26.
 DR N-PSDB; Q49155.
 XX
 PT DNA segments encoding monoclonal antibody - which binds to gp120
 PT and neutralises HIV, for treating AIDS, and for diagnosing and
 PT monitoring HIV infection
 XX
 PS Claim 10; Page 79; 10pp; English.
 XX
 CC mRNA from the known hybridoma F105 was converted to cDNA and this
 CC subjected to PCR amplification using primers corresp. to appropriate

CC parts of the heavy or light chains and having restriction sites to
 CC permit cloning. The extension prods. were isolated and sequenced.
 CC The recombinant human monoclonal antibody (Mab) binds to a
 CC discontinuous epitope on the HIV gp120 envelope glycoprotein, blocks
 CC the binding of gp120 to the CD4 receptor, and neutralises a broad
 CC range of HIV isolates. The Mab may be used to treat immune
 CC deficiency, esp. at doses of 0.1-10 mg/kg.

XX Sequence 129 AA;

XX

XX
PS Claim 1; page 87-88; 126pp; English.

XX
CC This sequence represents the human H11 monoclonal antibody variable (*V*)
CC region heavy (H) chain which specifically recognises the C antigen. Such
CC an antigen binding fragment may be used for treating a patient with
CC neoplasia. It is especially useful in the detection of lymphomas and
CC leukaemias where the tumour cells bearing the C antigen are circulating
CC in the patients bloodstream. The polynucleotide sequence may be used as a
CC primer or a probe and the encoded protein may be used in a vaccine or
CC for gene therapy. The human monoclonal antibody (Mab), designated H11,
CC specifically recognises cancerous cells. H11 is specific for
CC glioblastoma, neuroblastoma, malignant melanoma, breast adenocarcinoma,
CC lung adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and
CC prostate adenocarcinoma. The antigen binding fragment may also be used
CC to detect C-antigen in a sample.

XX
SQ Sequence 150 AA;

Query Match 80.3%; Score 494; DB 19; Length 150;
Best Local Similarity 81.0%; Pred. No. 1.8e-29;
Matches 98; Conservative 9; Mismatches 10; Indels 4; Gaps 2;

Oy 1 LWLPDITGETYMTQSATLSPGERATLGRASSVSSN LAWQOKPGQAPRILYGA 59
Db 17 lwlpidtgavtqsgptlspgeratlsrasvssylawqkpgqaprilya 76
Qy 60 STRANGIPARESGSGSTEFLTISLQSEFAVYQQINN--WPPYIFGQGKLEIK 116
Db 77 stratgmpdrisgsqtdftltislepedfavyycqqgssptpqitfggktveik 136
Qy 117 R 117
Db 137 r 137

Search completed: March 9, 2001, 16:43:36
Job time: 35 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 9, 2001, 16:44:01 ; Search time 23.59 Seconds

Perfect score: 615 US-09-203-768A-4

Sequence: 1 LWLDPDTGEIIMTQSATLS QYNNWNPYTFGQGTKEIKR 117 (without alignments)

Scoring table: BLOSUM62 336.769 Million cell updates/sec

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR-66;*

1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID

Description

ALIGNMENTS

RESULT 1

S40343 Ig kappa chain V-J region - human

C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40343
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891
A;Accession: S40343
A;Status: Preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-128 <KJF>
A;Cross-references: EMBL:X72453; NID:9441374; PID:9441375
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin F;36-110/Domain: immunoglobulin homology <IMM>

RESULT 2

Best Local Similarity 95.7%; Score 588.5; DB 2; Length 128;
Matches 114; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Query Match Description

OY 1 LWLDPDTGEIIMTQSATLSVSPGERATLSRASOVSSNIAWYQKPGAPRLIYGAS 60

Db 13 LWLDPDTGEIIMTQSATLSVSPGERATLSRASOVSSNIAWYQKPGAPRLIYGAS 72

QY 61 TRATGIPAREFSGSGNEFTLTISSQEDFAVYQCCQYNNWNPYTFGQGTKEIKR 117

Db 73 TRATGIPAREFSGSGNEFTLTISSQEDFAVYQCCQYNNW-PYTFGQGTKEIKR 128

RESULT 3

Best Local Similarity 95.7%; Score 588.5; DB 2; Length 128;
Matches 114; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Query Match Description

S40362 Ig kappa chain - human

C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40362
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891
A;Accession: S40362
A;Status: Preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-117 <KJF>
A;Cross-references: EMBL:X72472; NID:9441412; PID:9441413
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin F;26-100/Domain: immunoglobulin homology <IMM>

RESULT 4

Best Local Similarity 95.7%; Score 588.5; DB 2; Length 128;
Matches 114; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Query Match Description

S40362 Ig kappa chain - human

C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40362
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891
A;Accession: S40362
A;Status: Preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-117 <KJF>
A;Cross-references: EMBL:X72472; NID:9441412; PID:9441413
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin F;26-100/Domain: immunoglobulin homology <IMM>

RESULT 5

Best Local Similarity 95.7%; Score 588.5; DB 2; Length 128;
Matches 114; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Query Match Description

S40362 Ig kappa chain - human

C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40362
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891
A;Accession: S40362
A;Status: Preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-117 <KJF>
A;Cross-references: EMBL:X72472; NID:9441412; PID:9441413
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin F;26-100/Domain: immunoglobulin homology <IMM>

Query Match 93.4%; Score 574.5; DB 2; Length 117;
 Best Local Similarity 96.6%; Pred. No. 6.6e-41; 1;
 Matches 112; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 LWLDPDTGETIVMTQSPATLSPGERATLSCRASOSVSSNLAWYQOKPGQAPRLIYAS 60
 3 LWLDPDTGETIVMTQSPATLSPGERATLSCRASOSVSSNLAWYQOKPGQAPRLIYAS 62

RESULT 3
 S40328 Ig kappa chain - human
 C;Species: Homo sapiens (man)
 C;Date: 05-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C;Accession: S40328
 R;Klein, R.; Jaenichen, R.; Zachau, H.G.
 Bur. J. Immunol. 23, 3248-3271, 1993
 A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A;Reference number: S40312; MUID: 9408091
 A;Accession: S40328
 A;Status: preliminary;
 A;Molecule type: mRNA
 A;Residues: 1-331 <KLE>
 A;Cross-references: EMBL:X72438; NID:941344; PIDN:CAA51106.1; PID:941345
 C;Superfamily: Immunoglobulin V region; Immunoglobulin homology <IMM>
 Query Match 91.4%; Score 562; DB 2; Length 131;
 Best Local Similarity 89.7%; Pred. No. 7.9e-0; 5; Mismatches 7; Indels 0; Gaps 0;
 Matches 105; Conservative 103; Mismatches 103; Indels 0; Gaps 0;

QY 1 LWLDPDTGETIVMTQSPATLSPGERATLSCRASOSVSSNLAWYQOKPGQAPRLIYAS 60
 2 LWLDPDTGETIVMTQSPATLSPGERATLSCRASOSVSSNLAWYQOKPGQAPRLIYAS 71

Db 12 TRATGIPARFSGSGSGTEFTLISQLEDLATYYCQOYNDWPPWFGQGKVEIKR 128

RESULT 4
 S40378 Ig kappa chain - human
 C;Species: Homo sapiens (man)
 C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C;Accession: S40378
 R;Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A;Reference number: S40312; MUID: 9408091
 A;Accession: S40378
 A;Status: preliminary;
 A;Molecule type: mRNA
 A;Residues: 1-123 <KLE>
 A;Cross-references: EMBL:X72488; NID:941444; PIDN:CAA51155.1; PID:941445
 C;Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin F;29-103/Domain: immunoglobulin homology <IMM>
 Query Match 87.7%; Score 539.5; DB 2; Length 123;
 Best Local Similarity 87.3%; Pred. No. 5.3e-38; 6; Mismatches 8; Indels 1; Gaps 1;
 Matches 103; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 1 LWLDPDTGETIVMTQSPATLSPGERATLSCRASOSVSSNLAWYQOKPGQAPRLIYAS 60
 1 LWLDPDTGETIVMTQSPATLSPGERATLSCRASOSVSSNLAWYQOKPGQAPRLIYAS 65
 6 LWLDPDTGETIVMTQSPATLSPGERATLSCRASOSVSSNLAWYQOKPGQAPRLIYAS 65

RESULT 5
 A56701 Ig kappa chain V region precursor (HuA) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jan-2000
 C;Accession: A56701
 R;Nickerson, K.G.; Tao, M.H.; Chen, H.T.; Lerrick, J.; Kabat, E.A.
 J. Biol. Chem. 270, 12457-12465, 1995
 A;Title: Human and mouse monoclonal antibodies to blood group A substance, which are
 A;Reference number: A56701; MUID: 95279371
 A;Accession: A56701
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-128 <NFC>
 A;Cross-references: GB:LA1174; NID:9762823; PIDN:AAA64877.1; PID:9762824
 C;Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin F;36-110/Domain: immunoglobulin homology <IMM>
 Query Match 86.3%; Score 530.5; DB 2; Length 128;
 Best Local Similarity 88.0%; Pred. No. 3e-37; 7; Mismatches 7; Indels 1; Gaps 1;
 Matches 103; Conservative 103; Mismatches 7; Indels 1; Gaps 1;

QY 1 LWLDPDTGETIVMTQSPATLSPGERATLSCRASOSVSSNLAWYQOKPGQAPRLIYAS 60
 13 LWLDPDTGETIVMTQSPATLSPGERATLSCRASOSVSSNLAWYQOKPGQAPRLIYAS 72

Db 13 LWLDPDTGETIVMTQSPATLSPGERATLSCRASOSVSSNLAWYQOKPGQAPRLIYAS 72

QY 61 TRATGIPARFSGSGSGTEFTLISQLEDLATYYCQOYNDWPPWFGQGKVEIKR 117
 73 TRATGIPARFSGSGSGTEFTLISQLEDLATYYCQOYNDWPPWFGQGKVEIKR 128

RESULT 6
 R3HUCI Ig kappa chain precursor V-III region (CLL) - human
 C;Alternate names: Rheumatoid factor
 C;Species: Homo sapiens (man)
 C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 21-Jan-2000
 C;Accession: A01898
 R;Jirik, F.R.; Sorge, J.; Fong, S.; Heitzmann, J.G.; Curd, J.G.; Chen, P.P.; Goldfien
 Proc. Natl. Acad. Sci. U.S.A. 83, 2195-2199, 1986
 A;Title: Cloning and sequence determination of a human rheumatoid factor light-chain
 A;Reference number: A01898; MUID: 86177570
 A;Accession: A01898
 A;Molecule type: DNA
 A;Residues: 1-15 <TR>
 A;Note: the sequence was determined from the germline gene
 A;Genetics: C;Genetics: GDB:IGKV3
 A;Cross-references: GDB:136266
 A;Map Position: 2p12-2p11
 A;Introns: 17/1
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (lambda) chains disulfide bonded. In some cases, such as IgA and IgM, the subunits associate into
 C;Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C;Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-115/Product: rheumatoid factor; Ig kappa chain V-III region (CLL) #status predict
 F;21-43/Region: framework 1
 F;36-110/Domain: immunoglobulin homology <IMM>
 F;44-54/Region: complementarity-determining 1
 F;55-69/Region: framework 2
 F;70-76/Region: complementarity-determining 2
 F;77-108/Region: framework 3
 F;109-115/Region: complementarity-determining 3

F;43-108/disulfide bonds: #status predicted

Query Match

Best Local Similarity 85.7%; Score 527; DB 1; Length 115;

Matches 100; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LWLDPDTGETVMTQSPATLSVSPGERATLSRASOSVSSNLAQKPGQAPRLIYAS 60

Db 13 LWLDPDTGETVMTQSPATLSVSPGERATLSRASOSVSSNLAQKPGQAPRLIYAS 72

QY 61 TRATGIPAREFSGSGSGTEFTLTISSLQSEDFAVYCCQYNNWP 103

Db 73 TRATGIPAREFSGSGSGTEFTLTISSLQSEDFAVYCCQYNNWP 115

RESULT 7

S34005 Ig kappa chain V region - human

C;Species: Homo sapiens (man)

C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C;Accession: S34005; S30524

R;Marieette, A.; Brouet, J.C.

Bur. J. Immunol. 23, 846-851, 1993

A;Title: Nucleotideic sequence analysis of the variable domains of four human monoclonal

A;Reference number: S34001; MUID:93209281

A;Accession: S34005

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-107 <M&gt;

A;Cross-references: EMBL:Z18330

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.6%; Score 526.5; DB 2; Length 107;

Best Local Similarity 96.3%; Pred. No. 5.5e-37; Mismatches 1; Indels 1; Gaps 1;

Matches 104; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 9 EIVMTPSPATLSVSPGERATLSRASOSVSSNLAQKPGQAPRLIYAS 68

Db 1 EIVMTPSPATLSVSPGERATLSRASOSVSSNLAQKPGQAPRLIYAS 60

QY 69 RFSGSGSGTEFTLTISSLQSEDFAVYCCQYNNWPYTFGGTKIEIK 116

Db 61 RFSGSGSGTEFTLTISSLQSEDFAVYCCQYNNWPYTFGGTKIEIK 107

RESULT 8

S30553 Ig kappa chain precursor V-III region (Hah) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-Jan-2000

C;Accession: A30553

R;Liu, M.F.; Robbins, D.L.; Crowley, J.J.; Sinha, S.; Kozin, F.; Kipps, T.J.; Carson, D.

J. Immunol. 142, 688-694, 1989

A;Title: Characterization of four homologous L chain variable region genes that are rela

A;Reference number: A30553; MUID:8093959

A;Accession: A30553

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-115 <L&gt;

A;Note: the sequence was determined from the differentiated gene

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.4%; Score 525.5; DB 2; Length 144;

Best Local Similarity 87.2%; Pred. No. 8.8e-37; Mismatches 7; Indels 1; Gaps 1;

Matches 102; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

QY 1 LWLDPDTGETVMTQSPATLSVSPGERATLSRASOSVSSNLAQKPGQAPRLIYAS 60

Db 13 LWLDPDTGETVMTQSPATLSVSPGERATLSRASOSVSSNLAQKPGQAPRLIYAS 72

QY 61 TRATGIPAREFSGSGSGTEFTLTISSLQSEDFAVYCCQYNNWPYTFGGTKIEIK 117

Db 73 TRATGIPAREFSGSGSGTEFTLTISSLQSEDFAVYCCQYNNWPYTFGGTKIEIK 128

RESULT 10

B26555 Ig kappa chain V-III region (Ger) - human

C;Species: Homo sapiens (man)

C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 21-Jan-2000

C;Accession: B26555

R;Middaugh, C.R.; Littman, G.W.

J. Biol. Chem. 262, 3671-3673, 1987

A;Title: Atypical glycosylation of an IgG monoclonal cryoimmunoglobulin.

A;Reference number: A92630; MUID:8713766

A;Accession: B26555

A;Molecule type: protein

A;Residues: 1-116 <MD>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.0%; Score 523; DB 2; Length 116;

Best Local Similarity 91.7%; Pred. No. 1.1e-36; Mismatches 4; Indels 0; Gaps 0;

Matches 100; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 9 EIVMTPSPATLSVSPGERATLSRASOSVSSNLAQKPGQAPRLIYAS 68

Db 1 DIVMTPSPATLSVSPGERATLSRASOSVSSNLAQKPGQAPRLIYAS 60

QY 69 RFSGSGSGTETFLTISLQSEDFAVYCCQYNNWPPYTFGGTKEIKR 117
 Ig kappa chain V-J region - human
 C;Species: Homo sapiens (man)
 C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
 C;Accession: JE0244
 R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.
 R;Klein, R.; Jenichen, R.; Zachau, H.G.
 Bur. J. Immunol. 23, 3248-3271, 1993
 A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A;Accession: S40326
 A;Status: preliminary; translation not shown
 A;Residues: 1-110 <KLE>
 A;Reference number: S40312; MUID:9408091
 A;Molecule type: mRNA
 A;Cross-references: EMBL:X72436
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;32-106/domain: immunoglobulin homology <IMM>

Query Match 84.9%; Score 522; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 1.3e-36; Mismatches 0; Indels 0; gaps 0;
 Matches 101; Conservative 0; Mismatches 0; Indels 0; gaps 0;

QY 1 LWLPLDTGETMTOQSPATLSVSPGERATLSCRASQSVSSNLAWYQOKPGQAPRLIYGS 60
 Ig kappa chain V-J region - human
 C;Species: Homo sapiens (man)
 C;Accession: S40379
 C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 R;Klein, R.; Jenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A;Reference number: S40312; MUID:9408091
 A;Accession: S40379
 A;Status: preliminary; translation not shown
 A;Molecule type: mRNA
 A;Cross-references: EMBL:X72489; PIDN:9441446; PIDN:CAA51157.1; PID:9441447
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;36-110/domain: immunoglobulin homology <IMM>

Query Match 84.3%; Score 518.5%; DB 2; Length 128;
 Best Local Similarity 85.5%; Pred. No. 3e-36; Mismatches 8; Indels 1; Gaps 1;
 Matches 100; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY 1 LWLPLDTGETMTOQSPATLSVSPGERATLSCRASQSVSSNLAWYQOKPGQAPRLIYGS 60
 Ig kappa chain V-J region - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C;Accession: S40326
 R;Klein, R.; Jenichen, R.; Zachau, H.G.
 Bur. J. Immunol. 23, 3248-3271, 1993
 A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A;Accession: S40312; MUID:9408091
 A;Status: preliminary; translation not shown
 A;Residues: 1-110 <KLE>
 A;Reference number: S40312; MUID:9408091
 A;Molecule type: mRNA
 A;Cross-references: EMBL:X72436
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;16-90/Domain: immunoglobulin homology <IMM>

RESULT 12

S40379 Ig kappa chain V-J region - human
 C;Species: Homo sapiens (man)
 C;Accession: S40379
 C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 R;Klein, R.; Jenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A;Reference number: S40312; MUID:9408091
 A;Accession: S40379
 A;Status: preliminary; translation not shown
 A;Molecule type: mRNA
 A;Cross-references: EMBL:X72489; PIDN:9441446; PIDN:CAA51157.1; PID:9441447
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;36-110/domain: immunoglobulin homology <IMM>

Query Match 83.6%; Score 514; DB 2; Length 215;
 Best Local Similarity 89.9%; Pred. No. 1.2e-35; Mismatches 5; Indels 0; gaps 0;
 Matches 98; Conservative 5; Mismatches 6; Indels 0; gaps 0;

QY 9 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQOKPGQAPRLIYGS 68
 Ig kappa chain V region (60.3 hybridoma) - human
 C;Species: Homo sapiens (man)
 C;Accession: S4110; M29527
 R;Walls, M.A.; Hsiao, K.; Harris, T.J.
 Nucleic Acids Res. 21, 221-229, 1993
 A;Title: Vectors for the expression of PCR-amplified immunoglobulin variable domains
 A;Reference number: S34110; MUID:93324379
 A;Accession: S34110
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: mRNA
 A;Cross-references: EMBL:Z17330; PID:938511; PIDN:CAA8978.1; PID:g38512
 A;Note: human sequences cloned and sequenced prior to expression in mouse myeloma cell
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992
 C;Genetics:
 A;Introns: 17/1
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;36-110/domain: immunoglobulin homology <IMM>

Query Match 83.5%; Score 513.5%; DB 2; Length 129;
 Best Local Similarity 85.5%; Pred. No. 7.7e-36; Mismatches 6; Indels 1; Gaps 1;
 Matches 100; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 LWLPLDTGETMTOQSPATLSVSPGERATLSCRASQSVSSNLAWYQOKPGQAPRLIYGS 60
 Ig kappa chain V-J region (T33-5) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
 C;Accession: S46375; S38648
 R;Bensimon, C.; Chastagner, P.; Zouali, M.
 EMBO J. 13, 2951-2962, 1994

RESULT 13

JE0244

A;Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rea
A;Reference number: S46369; MUID:94313975
A;Accession: S46375
A;Molecule type: mRNA
A;Residues: 1-114 <BEN>
A;Cross-references: EMBL:Z27176; NID:9415967; PIDN:CAA81700.1; PTID:9415968
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;20-95/Domain: immunoglobulin homology <IMM>

Query Match 83.2%; Score 511.5; DB 2; Length 114;
Best Local Similarity 86.8%; Preq. No. 1e-35;
Matches 99; Conservative 8; Mismatches 6; Indels 1; Gaps 1;
Qy 5 DTTGEIWMSPATVSPPGERATSCRAQSOSVSN-LAWYQKPGQAPRLIVGASTRA 63
Db 1 DTTGEIWMSPATVSPPGERATSCRAQSOSVSN-LAWYQKPGQAPRLIVGASTRA 60
Qy 64 TGIPARFSGSGSGTFTLTISSQEDFAVYVCQYNNWPPYTFQOGTKLEIKR 117
Db 61 TGIPARFSGSGSGTFTLTISSQEDFAVYVCQYNNWPPYTFQOGTKLEIKR 114

Search completed: March 9, 2001, 16:44:01
Job time: 60 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on:

March 9, 2001, 16:46:04 ; Search time 14.74 Seconds

Sequence: 1 LWLDPDTGETVMTQSPATLS.....QINNNWPYPYTFGQGTKEIKR 117
256.337 Million cell updates/sec

Title: US-09-203-768a-4

Perfect score: 615

Scoring table: BioSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID

Description

KV3H_HUMAN

STANDARD;

PRT;

129 AA.

ID KV3H_HUMAN

AC P04207;

DT 20-MAR-1987 (Rel. 04 Created)

CC 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-III REGION CLL PRECURSOR (RHEUMATOID FACTOR).

OS Homo sapiens (Human)

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Butheria; Primates; Catarhini; Hominidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=8617757; PubMed=3083417;

RA Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,

RT Goldfien R., Carson D.A.,

RT "Cloning and sequence determination of a human rheumatoid factor light-chain gene." ;

CC Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).

RL RP SEQUENCE FROM N.A.

CC DR MEDLINE=8617757; PubMed=3083417;

RA Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,

RT Goldfien R., Carson D.A.,

RT "Cloning and sequence determination of a human rheumatoid factor light-chain gene." ;

CC Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).

CC DR INTERPRO: IPR0033006; -.

CC DR PFAM: PF00047; Ig; 1;

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 129

FT CHAIN 21 43

FT DOMAIN 44 54

FT DOMAIN 55 69

FT DOMAIN 70 76

FT DOMAIN 77 108

FT DOMAIN 109 118

FT DOMAIN 119 129

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CC EMBL: M12740; AA59992.1; -.

DR PIR; A01698; K3HNUC;

DR HSSP; P01789; 2MCP.

DR INTERPRO: IPR0033006; -.

DR PFAM; PF00047; Ig; 1;

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 129

FT CHAIN 21 43

FT DOMAIN 44 54

FT DOMAIN 55 69

FT DOMAIN 70 76

FT DOMAIN 77 108

FT DOMAIN 109 118

FT DOMAIN 119 129

FT DOMAIN 120 129

FT DOMAIN 121 129

FT DOMAIN 122 129

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FT DOMAIN 297 129

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CC EMBL: X02125; --; NOT_ANNOTATED_CDS.
 CC HSSP: P01789; 2MCP.
 DR INTERPRO: IPR00306; --.
 DR PTR: A01901; K3HUVH.
 DR PFM: PF00047; 1g; 1.
 DR KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 >16 IG KAPPA CHAIN V-III REGION VH.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 56 70 FRAMEWORK 2.
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 78 109 FRAMEWORK 3.
 FT DOMAIN 110 116 COMPLEMENTARITY-DETERMINING 3.
 FT DISULFID 43 109 BY SIMILARITY.
 FT NON_TER 116 116 116 AA; 12757 MW; 51CD55BA53B21929 CRC64;
 SQ SEQUENCE

Query Match 74.6%; Score 458.5; -DB 1; Length 116;
 Best Local Similarity 87.5%; Pred. No. 6.2e-38;
 Matches 9; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

Qy 1 LWLPLDTGEVLMVSPATLVSVSPGERATLSCRASQVSN-LAWYQKPGQAPRLIYGA 59
 Db 13 LWLPLDTREIYVMTQSPPTLSSLRGERVTLSCRASQVSSSYLTWYQKPGQAPRLIYGA 72

Qy 60 STRATGIPARFSGGGSGTPEFTLTISLQSEDFAVYQCOQYNNWP 103
 Db 73 STRATSIPIRFSGSGSGTDFLTISLQEDFAVYQCOQDHNL 116

RESULT 8
 KV3B_HUMAN
 ID KV3B_HUMAN STANDARD; PRT; 109 AA.
 AC P01620;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE IG KAPPA CHAIN V-III REGION SITE.
 OS Homo sapiens (Human); Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-72188439; PubMed=5027703;
 RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
 TI). IV. The complete amino acid sequence and its significance for
 the mechanism of antibody production.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
 CC -- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR: A01789; K3HUVH.
 DR HSSP: P01789; 2MCP.
 DR INTERPRO: IPR00306; --.
 DR PFM: PF00047; 1g; 1.
 DR KW Immunoglobulin V region; Bence-Jones protein.
 FT DISULFID 23 89
 FT NON_TER 109 109 BY SIMILARITY.
 SQ SEQUENCE 109 AA; 11788 MW; 8C35058CDC7749BC CRC64;

Query Match 73.0%; Score 449; DB 1; Length 109;
 Best Local Similarity 81.8%; Pred. No. 4.8e-37;
 Matches 90; Conservative 10; Mismatches 8; Indels 2; Gaps 2;

Qy 9 EIVMTQSPATLVSVSPGERATLSCRASQVSN-LAWYQKPGQAPRLIYGA STRATGIP 67
 Db 1 EIVMTQSPATLSSLRGERVTLSCRASQVSN-LAWYQKPGQAPRLIYGA STRATGIP 60

Qy 68 ARFGSGSGTPEFTLTISLQSEDFAVYQCOQYNNWP 117
 Db 61 DRFGSGSGTDFLTISLQEDFAVYQCOQYNNWP 109

RESULT 10
 KV3E_HUMAN
 ID KV3E_HUMAN STANDARD; PRT; 109 AA.
 AC P01623;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE IG KAPPA CHAIN V-III REGION WOL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-82046598; PubMed=6794615;
 RA Andrews D.W.; Capra J.D.;
 RT "Amino acid sequence of the variable regions of light chains from two
 idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
 group. ";
 RL Biochemistry 20:5816-5822(1981).
 CC --!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IgM WITH ANTI-GAMMA
 CC GLOBULIN ACTIVITY.
 DR PIR: A01892; K3HUST.
 DR HSSP: P01789; 2MCP.
 DR INTERPRO: IPR00306; --.
 DR PFM: PF00047; 1g; 1.
 DR KW Immunoglobulin V region.
 FT DISULFID 23 89
 FT NON_TER 109 109 BY SIMILARITY.
 SQ SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;

Query Match 73.8%; Score 454; DB 1; Length 109;
 Best local similarity 82.7%; Pred. No. 1.6e-37;

RT group;"

RL Biochemistry 20:5816-5822(1981).

CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.

DR PIR; A01896; K3HUBL.

DR HSSP; P0189; 2NCP.

DR INTERPRO; IPR003006; -.

DR PFAM; PF0047; Ig; 1.

KW Immunoglobulin V region.

FT DISULFID 23 89 NON_TER 109 109 SEQUENCE 109 AA; 11746 MW; 566C115EBB9CBFEE CRC64; 61 DRFSGSGSGDFTLTLISRLPEDFAVYCOQYSL-GRTFGQGTKEIKR 109

RESULT 11 KV3A_HUMAN STANDARD; PRT; 108 AA.

ID KV3A_HUMAN STANDARD; PRT; 108 AA.

AC P01619; 1] DT 21-JUL-1986 (Rel. 01, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DE 15-JUL-1999 (Rel. 38, Last annotation update)

OS Homo sapiens (Human).

OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]

RP SEQUENCE.

RX MEDLINE=77038198; PubMed=624717;

RA Capra J.-D.; Klapser D.G.;

RT "Complete amino acid sequence of the variable domains of two human IgM anti-gamma globulins (Lay/Pom) with shared idiotypic specificities";

RT Scand. J. Immunol. 5:677-684(1976).

CC -!- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN, WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.

CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.

DR PIR; A01871; K3HUBL.

DR HSSP; P01607; IREI.

DR INTERPRO; IPR003006; -.

DR PFAM; PF0047; Ig; 1.

KW Immunoglobulin V region.

FT DOMAIN 1 23 FRAMEWORK 1.

FT DOMAIN 24 34 FRAMEWORK 2.

FT DOMAIN 35 49 FRAMEWORK 3.

FT DOMAIN 50 56 FRAMEWORK 4.

FT DOMAIN 57 88 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING 3.

FT DISULFID 23 88 BY SIMILARITY.

FT NON_TER 108 108 SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 70.8%; Score 43.5; DB 1; Length 108; Best Local Similarity 73.4%; Pred. No. 9.7e-36; Matches 80; Conservative 16; Mismatches 12; Indels 1; Gaps 1;

QY 9 EIVMOPSPATLSVSGERATLSCRASQSVSSN-LAWYQOKPGQARPLILYGASTRATGIP 68

Db 1 DIQMTQSPSSLSVSVQDRVTITCQASQVNVALNLYQOKPGQAPRLILYGASTRAGVPS 60

QY 69 RFGSGSGTETFTLTLISLQSDPFAVYCOQYNNWPPYTFGQGTKEIKR 117

Db 61 RFSGSGSGDFTFTLQLPBDIATYCOQYNNWPP-TFGQGTKEIKR 108

RESULT 13 KV4C_HUMAN STANDARD; PRT; 134 AA.

ID KV4C_HUMAN STANDARD; PRT; 134 AA.

AC P06314; 1] DT 01-JAN-1988 (Rel. 06, Created)

DT 01-APR-1988 (Rel. 07, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE 15-JUL-1999 (Rel. 38, Last annotation update)

IG KAPPA CHAIN V-IV REGION B17 PRECURSOR.

OS Homo sapiens (Human).

OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]

RP SEQUENCE FROM N. A.

RX MEDLINE=80041854; PubMed=2997713;

RA Marsh P.; Mills F.; Gould H.;

RT "Detection of a unique human V kappa IV germline gene by a cloned cDNA probe";

RT Nucleic Acids Res. 13:6531-6544(1985).

RN [2]

RP REVISION TO 76.

RA Marsh P.;

RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.

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RESULT 12 KV1M_HUMAN STANDARD; PRT; 108 AA.

ID KV1M_HUMAN STANDARD; PRT; 108 AA.

AC P01605; 1] DT 21-JUL-1986 (Rel. 01, Created)

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us-09-203-768a-4.rsp

Page 7

Qy	115	IKR	117
	111		
Db	131	IKR	133

Search completed: March 9, 2001, 16:46:05
Job time: 179 sec

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Om protein - protein search, using sw model

Run on: March 9, 2001, 16:46:47 ; Search time 38.3 Seconds
(without alignments)
358.050 Million cell updates/sec

Title: US-09-203-768A-4

Perfect score: 615

Sequence: LNWUPDTGEIVMTQSATLS.....QYNNNPPYTFGGCTKLEIKR 117

Scoring table: BLOSUM62

Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRMBL15:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_primate:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	529	86.0	109	4	Q9UL85
2	513.5	83.5	108	4	Q9UL85
3	449	73.0	109	4	Q9UL78
4	431	70.1	109	4	Q9UL86
5	425.5	69.2	108	4	Q9UL79
6	394.5	64.1	108	4	Q9UL70
7	390.5	63.5	108	4	Q9UL77
8	378	61.5	107	4	Q9UL81
9	357.5	58.1	298	11	Q9QYFO
10	352.5	57.3	114	4	Q9UL80
11	345	56.5	214	11	Q9RL1AS
12	345	56.1	106	5	Q9A410
13	340.5	55.4	99	11	Q9JL74
14	333.5	54.2	101	11	Q9JL78
15	318.5	51.8	97	11	Q9JL76
16	318.5	51.8	103	11	Q9JL80
17	316.5	51.5	107	11	Q9JL84
18	310.5	49.1	104	11	Q9JL82
19	288.5				Q9N0W5 oryctolagus

RESULTS

RESULT ID	PRELIMINARY;	PRT;	109 AA.
Q9UL85	Q9UL85;		
	DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
	DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)		
	DE MYOSIN REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).		
	OS Homo sapiens (Human).		
	OC Eukaryota; Metazoa; Chordata; Crania; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
	OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
	OX NCBI_TaxID=9606;		
	RN [1]		
	RP SEQUENCE FROM N.A.		
	RX MEDLINE=98271139; PubMed=2614934;		
	RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;		
	RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.", Clin. Immunol. Immunopathol. 87:184-192(1998).		
	DR EMBL; AF035029; AAD56265.1; -.		
	DR INTERPRO; IPR03006; -.		
	DR PFAM; PF00047; ig: 1.		
	DR HSSP; P01607; IRET.		
	DR FT NON_TER 1 109 109		
	DR SEQUENCE 109 AA: 11761 MW: FB1E43E7C7AFACC CRC64;		

ALIGMENTS

Query Match 86.0%; Score 529; DB 4; Length 109;
Best Local Similarity 92.7%; Pred. No. 2, 5e-47;
Matches 101; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 9 ETWMTSPATSVSPGRATLCSRASQVSNTLAWQKPGQAPRLIYGSSTRATGIPA 68
Db 1 EIWMTSPATSVSPGRATLCSWASQSISSNLAWIQQPKPGQAPRLIYGSSTRATGIPA 60

Qy 69 RSGSGGCTEFLITISLQSEDFAVYQCOQNNPPYTFGGCTKLEIKR 117
Db 61 RPSGSGGCTEFLITISLQSEDFAVYQCOQNSWPLTEGGTKVEIKR 109

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us-09-203-768a-4.rspt